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QY 380 AsnAspIleAspValGluProGlnPheAspPheLeuValIleIysAspGlyAlaThrAla 399
Db 2729 AATCATTTTGTGATGTGAGCCCATTTGACTTTCTCCGGGTCAAGAGATGATGCACTTCT 2788
QY 400 GluAlaIleProValleuGlyThrPheSerGlyAsnGlnleuProSerSerIleThrSerSer 419
Db 2789 GACATTAACGTCTCGGTGACTTTTCTGCGCATGAGTGCCTTCCAGCTGCCAGAGT 2848
QY 420 GlyHisValAlaArgLeuGluPheGlnThrAspHisSerThrGlyIleAspGlyPheAsn 439
Db 2849 GGGCATATAGTCCCTGGAATTTCACTGTCACATTCCTCACTAGTCCAGAGGTTAAAC 2908
QY 440 IleThrPheThrThrPheArgHisAsnGluCysPheAspProGlyValProValAsnGly 459
Db 2909 ATCATTTACACACNTTTGGTCAAGAAATGAGTGCATGATCCTGGCATTCCTATTAACGGA 2968
QY 460 LysArgPheGlyAspSerLeuGlnleuGlySerSerIleSerPheLeuCysAspGluGly 479
Db 2969 CGAGGTTTGGTGAAGGTTTCTAATCGGAGCTCGGTCTTCTTCCACTGTGATGATGCG 3028
QY 480 PheLeuGlyThrGlnGlySerGluThrIleThrCysValleuIleuIleGlySerValVal 499
Db 3029 TTTGTCAAGACCCAGGATCGAGTCCATTAACCTGCACTGCAAGCGGAAAGTGTGTC 3088
QY 500 TrpAsnSerAlaValLeuArgCysGluAlaProCysGlyGlyHisleuThrSerProSer 519
Db 3089 TGGAGCTCCACCGGCCCCCTGTGAACTCAATGTGTGACATCTGACAGCGTCCAGC 3148
QY 520 GlyThrIleLeuSerProGlyTrrProGlyPheThrIleAspAlaLeuSerCysAlaTrr 539
Db 3149 GGAATCTTTTGGCTCTGATGAGTGCAGATATTAAGAAATCTTAACTGTGAATGAG 3208
QY 540 ValIleGluAlaGlnProGlyTrrProIleIleIleThrPheAspArgPheIleThrGlu 559
Db 3209 ATATATGAACCAAAACAGGCACTCTATCAAAATACTTTGACAGATTTGACAGACAG 3268
QY 560 ValAsnThrAspThrLeuGluValAlaAspGlyIleArgThrIleSerAlaProLeuIleGly 579
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QY 600 LeuPheSerThrAspIleSerHisSerAspIleGlyPheGlnleuArgIleGluThrIle 619
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QY 640 AsnAspPheThrValGlyAlaLeuValThrPheSerCysAspSerGlyThrThrLeuSer 659
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QY 700 ProAspPheThrProAsnleuAsnCysThrTrpIleIleGluThrSerHisGlyIle 719
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Qy 2011 -----CysProPro-----ThrIleLeuProAsnAla 2020
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Qy 2021 GluValValThrGluAsn 2026
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RESULT 6
US-10-276-934-3
Sequence 3, Application US/10276934
Publication No. US20030180750A1
GENERAL INFORMATION:
APPLICANT: University of Leeds
APPLICANT: Markham, Alexander F.
APPLICANT: Jackson, Andrew P.
APPLICANT: Woods, Christopher G.
FILE OF INVENTION: Treatment of Cancer and Neurological Diseases
TITLE REFERENCE: 9052-144
CURRENT APPLICATION NUMBER: US/10/276,934
PRIOR FILING DATE: 2002-11-20
PRIOR APPLICATION NUMBER: PCT/GB01/02240
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: GB0012186.3
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 6409
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:

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NAME/KEY: misc feature
LOCATION: (588)..(588)
OTHER INFORMATION: "n" is any nucleotide
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NAME/KEY: misc feature
LOCATION: (672)..(672)
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LOCATION: (1265)..(1265)
OTHER INFORMATION: "n" is any nucleotide
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NAME/KEY: misc feature
LOCATION: (6387)..(6387)
OTHER INFORMATION: "n" is any nucleotide
US-10-276-934-3

Alignment Scores:
Pred. No.: 0
Score: 7610.50
Percent Similarity: 79.70%
Best Local Similarity: 65.74%
Query Match: 44.81%
DB: 15 Gaps: 10

US-10-016-248-2 (1-3104) x US-10-276-934-3 (1-6409)
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Db 126 ACCCATMAAACTGTCTGCGCATATGAAATTAACATCAACCATGATCCGAGAGCA 185
Qy 62 -----LeuThrGln-ValGlyValSerGlnI 70
Db 186 TAGCTTATATGATCTCGGAAACCATGCTTCATGAAATTCAGATGAGCAAGG 245
Qy 70 Y-----HisAsnMetCysProAspProGlyIleProGlyValArg 85
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Qy 125 AspHisArgProValCysArgAlaArgMetCysAspAlaHisIleuArgGlyProSerG 145
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Qy 185 uArgGlyTyrAspThrIleuThrValGlyAspGlyGlyGlnAspGlyAspGlnLysThrVa 205
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		858 CCATGGAGATACACTCACCTTGGATGCGCGGCGGCTTTGAGCTGTGGGGGAGAGAGT		917
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Oy	1158	CATTCTGACATATCTGTCTGGATCTTTTCTGGCAATGAAGTCCCTCCAGCTGGC		1217
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		1218 CAGCAGTGGGCATATAGTTGCTTGGATTCAGTCTGACATTCACACTGCGAGAGG		1277
Oy	437	yPheAsnIleThrPheThrTrhPheArgHlAsnGluCybProAspProGlyValProVa		457
Db	1278	GTTCAACATCACTTACACCACTTGTGTGAGMATAGGCCATGATCTCGCAATTCAT		1337
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Db	1338	AAAGCGACGACGTTTGGTGCAGGTTCTACTCGGAGCTCGGTTCTTTCACACTGGA		1397
Oy	477	pGluGlyPheLeuGlyTrhGlnGlySerGlyTrhIleThrCybValLeuLybGluGlySe		497
		1398 TGATGGCTTTGTCAGACCCAGGAGTCCGAGTCCATTACTGCAATCGCAAGACGGAA		1457
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Oy	1518	GTCCACGGAGTCATTTGGCTCTCGAATGGCCAGAGATTTATTAAGATCTTTTCATTTG		1577
Db	537	sAlaTrpValIleGluAlaGlnProGlyTybProIleLybIleThrPheAspArgPheLy		557
		1578 TGAATGGATATATGAAGAAAACAAGGCCACTATCAAAATATCTTTGACAGATTCCA		1637
Oy	557	sThrGluValAsnTybAspThrLeuGluValArgAspGlyArgThrTybSerAlaProLe		577
Db	1638	GACAGAGGTCAATTTTGACACTTGTGAGTCAAGATATGGCGACGACATTTGTCTCCACT		1697

QY	577	IIISGLYVALTYRTHISGLYTHRGINVALPROGHNPHLEUILLSETHSERANTRYLE	597
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QY	597	UTRYLEULEUHPHESETHRAPPLYSERHISERASPILSGLYPHEGLNLEUARGTRYGL	617
DB	1758	CTACTGCTATTCACACTGACCAACACCGGTCAGATCGGCTTCTCATTCACATATGA	1817
QY	617	UTRTHLETHRLEUGLNSETHAPHSICYLEUASPPIROGLYILEPROVALANGIYNAR	637
DB	1818	GAGGTGACGGCTTAGTCGGAATTCCTCCGTGACCGCGGATCCCTGTGAACGGCCATCG	1877
QY	637	GHSGLYASNNAPHERYRVALGLVALALEUVALTHPHESECYASPSERGTRYRTH	657
DB	1878	CCACGGTGGAGACTTTGGCATCAGGTCCACAGTACTTTAGCTGTACCCGGGGTACAC	1937
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QY	697	OGLYPHEPROASPHERYRPROASNANLEUASCYETHTRIPLEILEIUGLTHRSETHI	717
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QY	717	SGLYLYSGIYVALPHEPHERTHPEHISTHRPHEHILEUGLNUSEGLYHISAPTRYLE	737
DB	2118	TGGGAAAGGAGTTCAATATGATCTTTCACACCTTTCACCTTGAGAGTTCACACGACTATT	2177
QY	737	ULEUILLETHRCIUNANGIYSERPETHRGINPROLEUARGIUNETHRGISERAGYLE	757
DB	2178	ACTGATCACAGAGATGGAATTTTCCAGACCCCTTGCCAGGCTCACCGGGTCGT	2237
QY	757	UPROALAPROLESERIAGILEURYGLYASNPHETHRALAGIYNALRGPHEIIESE	777
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QY	777	RASPHERSETHSERTRYGLIUGLYPHEANILLETHPHESEGLUNYRTRAPLEUGIUPR	797
DB	2298	AGACTCTTCAATTTTCGACGAGGCTTCATATCACATTTTCAGAAATATGACCTGGAGCC	2357
QY	797	OCYSGIUGLUPROGLUNVALPROAIATRYSERILEARGLYSGIYLEUGLNPHGLIYALGI	817
DB	2358	ATGTGATGATCTGTGAGATCCCTGCTTCAGCGAAGAAATGGTTTCACTTGGTGTGGG	2417
QY	817	YASPTHRLEUTHRPHSESECYSPHEPROGLIYTRYARGLEUGLNYTHRALARGILETH	837
DB	2418	AGACTCTCTGACGTTTTCCTGCTTCCGCGGATATCGTTTGAAGGTCCACCAAGCTTAC	2477
QY	837	ICYLEUGLIGLYARGARGARGLEUUTPSESEPROLEUPROARGCYVALIAGIUCY	857
DB	2478	CTGCTCGGTGGGGGCGCGCCTGTGTGTGATGACCTCTGCCAAGATGTGTGGCCGATG	2537
QY	857	SGIYASNSERVALTHRGIYTHRGINGIYTHRLEULEUSERPROASNPHEROVALAENTY	877
DB	2538	TGGAGCAAGTGTCAAGGAATGAAAGAACATTACTGTCTCCAAATTTTCCATCATATTA	2597
QY	877	RASNNASNNHISGLUCYRIETRYSERILEGINTHGLNPROGLIYVSGIYILEGLNLE	897
DB	2598	TGAATATATACATAGGTATCTATAAATAAGAAACGAAGCGGCAAGGACATCCACT	2657
QY	897	ULVALAARGIAPHEGLNLEUSERGIUGIYASPVALLLEULYSEVALTRYASPGIYANAS	917
DB	2658	TAGAAACAGAACTTCCAGCTGTTTGAAGGAGATCACTTAAAGGTATATGATGGAAGA	2717
QY	917	NASNSERIALARGLEULEUGIYVALPHESETHISERGIUMETMEGLYVALTHIRLEUS	937
DB	2718	CAGTTTCTCAAGTCCAGTCCGAGCTTCAATAAAGAACTTGGGGGTGATCTCAAA	2777

QY 937 nSerThSerSerSerLeuTrpLeuAspPhe11eThrAspAlaGluAenThrSerLysG1 957
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 QY 977 sPheG1yTrpLysValH1sAspGluG1yH1sPheAlaG1ySerSerLysSerPheSerCy 997
 Db 2898 CTAGGCTATAGAGATCCGTGATGAAAGGCCATTATACCACTGTAGTTCTGTACAGTTG 2957
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Db 5898 GGGCTATAGCTTCACCAACCAAGTCTCTCAAGTTCCACAGCGCATTTTCAAAATGAGAG 5957
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Qy 2018 oAsnAlaGluValValThrGluAsn 2026
Db 6078 TTCAGCCGAGGGCGGTATGATTTCT 6102

RESULT 7
US-10-276-934-1
; Sequence 1, Application US/10276934
; Publication No. US20030180750A1
; GENERAL INFORMATION:
; APPLICANT: University of Leeds
; APPLICANT: Markham, Alexander F.
; APPLICANT: Jackson, Andrew P.
; APPLICANT: Woods, Christopher G.
; TITLE OF INVENTION: Treatment of Cancer and Neurological Diseases
; FILE REFERENCES: 9052-144
; CURRENT APPLICATION NUMBER: US/10/276,934
; PRIOR FILING DATE: 2002-11-20
; PRIOR APPLICATION NUMBER: PCT/GB01/02240
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: GB0012186.3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 5598
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-276-934-1

Alignment Scores:
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Score: 7159.00 Matches: 1262
Percent Similarity: 81.17% Conservative: 264
Best Local Similarity: 67.13% Mismatches: 279
Query Match: 42.15% Indels: 75
DB: Gaps: 7

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Qy 165 eIleThrAlaLeuAsnProSerLYsValIleLYsLeuAlaPheGluGluPheAspLeuG1 185

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Db      736 -----CTGACGTGGATGATGATAGC----- 753
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DB	2718	CAGTTCCTCACGTCACAGTGGGACAGTTCACATAAAGAACTCTGGGGGCGTACCTTAA	2777
QY	937	NSETRTHSERSESERLEUTRPLEASPPHEILETHASPLAAGLUANTHSERLYSGI	957
DB	2778	CAGACATCTCCATACCTGCTGGCTAGAGTTCTAACACCAATGAGATCTACACCGACCAAG	2837
QY	957	YPHGELIUENHISPHESERSERPHEGULLEUILELYCYSGEGLUAPPROGILYTHPRPOLY	977
DB	2838	TTTTCACTACCTCATACAGTTTGTGATCTGTTAAATGTGAGATCCGGGCACTCCCTAA	2897
QY	977	APHGELYTRYLYEVALHISAPRGUIGYHISPHALAGLYSERSEVALSERPHESECY	997
DB	2898	CTACGGCTATATAGATTCGGTATGAAAGGCCACTTATACCGACACTAGTTCTGTACATGTTG	2957
QY	997	SAAPPROGILYTRYSERLEUATRGYISERGULUULEUCYALEUENUGLYGUAGAT	1017
DB	2958	CAACCCGGGGATGCCCATGATGCGACAGAACACCCCTGACCTGTTTGATGAGACAGAG	3017
QY	1017	GTHTRIPASPARPROLEUPROTHRCYVALALAGLYCYSGLYGILYHTRHIALAGLYGI	1037
DB	3018	AGTGTGGGACAAACACTACTCTTGCTGATGCGGAATGTGTGTGCAGATCCATGAGC	3077
QY	1037	UVALISERGLYNALLEUSERPROGILYTRYPROALAPROTYGILUHIISANLEUANCY	1057
DB	3078	CACATCAAGSAGAAATATGTTCCCTGGCTATCCAGCTCCGATACCAACCACTCCACTG	3137
QY	1057	SILETRIPTRHILEGULAGLUALAGLYCYETHRILEGLYUENHISPHLEUVALPHEAS	1077
DB	3138	CACCTGGATTTATAGGCGNACCCAGAAAGAACATTAGCTCCATTTCATGTGTTTCSA	3197
QY	1077	PTRHGLUGLUVALHISAPVALLEUASRGILETRIPSPGYPROVALISGUSERGLYAL	1097
DB	3198	CACGGAATGCGCTCACGACATCTCCAAAGTCTGGAGCGGGCGGTGACAGTGCATCTCT	3257
QY	1097	ULLEUUGLUENSERGYPROALALUUPROLYASPLUENHISETRHPHEANSRVA	1117
DB	3258	GCTAAGAGAGAGAGTGCTCGGCCCTTCCGAGAGACATCCACAGCACTTCAACTACT	3317
QY	1117	IVALLLEUGLNPHESETRHAPPPHEPETHSERLYEGLNGLYPHEALALEGINPHESE	1137
DB	3318	CACCTCGAGTTGCACAGCGACTTCTTCATACAGCAAGTCGGCTTCTCCATCCAGTTCTC	3377
QY	1137	FVALISERTHRALATHSERCYAANAPPROGILYILEPROGILNANGLYSERARGSGI	1157
DB	3378	CACCTCAATTGACACCACCTGTATACGATCCAGTATGCCCCAAATATGGACCCGCTATGG	3437
QY	1157	YASPSERTROJULIAGLYASPSERTHVALPHEGLICYASAPPROGILYTRYALALENGI	1177
DB	3438	AGACACAGAGAGGCTGGAGNACACCGTACATTCAGATGTGACCTCGCTATCAGCTCCA	3497
QY	1177	NGLYSERALAGLULESERCYVALYLVILEGLUASNAHQBHEHETROGINPROSEPR	1197
DB	3498	AGGACAAAGCCAAATATCACCTGTGTGACGAGTAATACCGGTCTTTTGGCAACGACACC	3557
QY	1197	OPROTHCYALILEALAPROCYSGLYGYASPLEUTHGLYPROSEGLYVALILEUENSE	1217
DB	3558	TCTCAACATGCACTCTGTTGTGAGGGAATCTACCGGGCCACAGACAGTGTATTTGTC	3617
QY	1217	RPROASNTYRPROGILYTRYPROGILYLYEGLICYASAPTRIPYVALTHVALSE	1237
DB	3618	ACCACACTACCCACAGCGGTATCTCTCGGGAAGGAATGTGATCGAGAGATTAAGTGAA	3677
QY	1237	RPROASPTYRVALILEALAUVALPHEASNTILEPHEANLEUGLUPROGILYTRYAPPH	1257
DB	3678	CCCGGACTTGTGTACCTGGCTGATTAACAAAGTTTCAACATGAGGCCACAGTATGACTT	3737

QY	1257	eleuH1s1lelyrtharpgllyrtaarpsrleuSerProleu11lelyserPheTyrglyse	1277
Db	3738	CCTACACATTCATATGAAAGGGAAGATTCCAAACGGCCCTCATTTGGAGTTTACAGGGCTC	3797
QY	1277	rg1leuaprod1yrgt1leg1uSerSerAasrleuPheleu1aPhearGserAs	1297
Db	3798	TCAGGCCCCCAAAAGAAATAGAGATAGCGAAACAGCTGTTTTGCCATTTCGGAATGA	3857
QY	1297	pa1aSerValserAna1aqlPheval11eapTyrrthgluaaBProarng1uSerCy	1317
Db	3858	TGCCTCGGTGGCCCTTTCAGGGCTTCGCGCATTTGAATTAAAGAGAAACACGGGAAGCTTG	3917
QY	1317	sPheapPProgl1ySer11elyBaang1ythrtaVal1GlyserApleu1yBleu1ySe	1337
Db	3918	TTTTGACCCCAAGAAATATTAATGAATGGACACAGAGTTGGAACACACTTCAAGCTTGGCTC	3977
QY	1337	rSerValthrTyrrCysh1sg1ygyTYrGluVal1Glu1yThrserrth1uSerCy	1357
Db	3978	CACCATCACCTTACAGGTGTGACTGTGGCTATTAATTTCTTGACCCCTCATTCATACCTG	4037
QY	1357	s11e1euG1yProaspG1yLysProval11rPaasnaBProarBProval1Cystr1a1aP	1377
Db	4038	TGTATTTGGGCTATGGGAAACCTCTCGGAGCAAGTGTGCTCCCTCGCAATGTCTCC	4097
QY	1377	oCyge1yG1yG1nTyrrVal1GlyserAepG1yVal1a1leuSerProaBnTyProgl1aB	1397
Db	4098	CTGTGAGGCGCAGATACACGGGATCAGAGGGGGTGTATTTCACCAACTACCCCACTAA	4157
QY	1397	nTyrrThSerG1yG1n11eCyBleuTyrrPheval1ThVal1ProlyaBapTyrrVal1a1P	1417
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QY	1417	eG1yG1nPhe1a1aPhePhe1s1rth1a1a1euaaBAsPVal1a1G1uVal1a1aBepG1yH1	1437
Db	4218	TGGACAGTTGGCTCATTTCCAGACAGCCCTGAAGATTGGCACAATATTGATGTGAAC	4277
QY	1437	sSerG1nH1sSer1a1rleu1euSerSer1euSerG1ySerH1sThrg1y1uSer1euPr	1457
Db	4278	CCATGACACAGCACTTCTCACCTCACTCTCGGGGTCTTCACCTCAGGGGAAACATTGGCC	4337
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QY	1477	gG1yPheH1sPheVal1TyrrG1n1a1aVal1ProarGThSer1a1aThrg1nCyseSer1a	1497
Db	4398	CGGCTTCACCTCTGTGATCAAGCTGTTCCTCGTACAGTACACCCCAATGCACTGTGT	4457
QY	1497	1Progl1uProarGTyrrG1yBArG1euG1ySerAsPpHeSerVal1a1a1a1eVal1a1r	1517
Db	4458	CCCCGAGCCAGATACGGAAAGAAATATGGTTCTGAGATTTTCTCGCGGCTCCATGCTGCG	4517
QY	1517	qPheG1uCyBaBserG1yTyrr1a1e1euG1nG1ySerProgl1u1eG1yB1euProva	1537
Db	4518	ATTGAGAGCAACCGGGATACCTGTTCAAGGTTCACGCGCGCTCCACCTGCAAGTCCGT	4577
QY	1537	1ProG1y1a1a1eu1aG1nTPaB1aValSer1a1a1aProThrCyB1a1a1aProCyB1yG1	1557
Db	4578	GCCCAACGCTTGGGACACGTGAAACGACACGATCCCAAGCTGTGTGATCCCTGCAATGG	4637
QY	1557	yAaB1euThrg1u1a1rG1yrr11e1euSerProG1yPheBProgl1uProTyrr1e1uAs	1577
Db	4638	CAATTTCACCTACGAAAGAGGTAACAATCTGTCCCGGCTTACCTGAGCATTCGAAA	4697
QY	1577	nSer1euBancYBAr1a1rBp1y11eVal1a1Progl1uG1y1a1aG1y11eG1n11eG1nVa	1597
Db	4698	CAACTTGAACGTATATAGGAAGATCAATGTTACGAGAGGCTCGGGGAATTCAAGATCCAGT	4757
QY	1597	1ValSerPheVal1Thrg1uG1nAaBTPAsPSe1euG1yVal1a1PheapG1y1a1a1aPAs	1617
Db	4758	GATCAGTTTTCACCGAGACGAACCTGGACTCCCTTGAGATTCACAGATGTGGGGATGT	4817
QY	1617	nThVal1Thr1e1euG1ySerPheSerG1yThThVal1a1a1e1eu1euB1e1rth	1637

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Db      4818 GACCCACCCAGACTGGAGCTTCTCAGGACCACTGACCGGACTGTCGAAACAGTAC
Qy      1637 rSerAnGlnLeuYrLeuHisPheTySerAspIleSerValSerIleAlaGlyPheH
Db      4878 TTCACCAACCTTACCTGACATTCCTGACATTCGATTCGATTCGATTCGATTCGATTC
Qy      1657 sLeuGlnTyRysThrValGlyLeuSerSerCyseProGluProAlaValProSerAnG
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Qy      1677 yValIysThrGlyGluATGTYrLeuValAsnAspValIserPheGlnCyseGluProG
Db      4998 CATCAAAATCGAGATCCGTCATGATGTAACGACGTCCTCTCTCCAGTCGAGCCCGG
Qy      1697 YTYrAlaLeuGlnGlyHisAlaHisIleSerCyseMetProGlyThrValAlaGAGTTPAS
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Qy      1737 lIleLeuSerProGlyPheProGlyAsnTYrProSerAsnMetAspCyseSerTyPylsI
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Qy      1817 eHisSerAspHisSerGlnAsnArgProGlyPheTyLeuGluTYrGlnAlaTYrGluLe
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Qy      1837 uGlnGluCyseProAspProGluProPheAlaAsnGlyIleValArgGlyAlaGlyTYrAs
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RESULT 8
US-10-276-934-2
; Sequence 2, Application US/10276934
; Publication NO. US20030180750A1
; GENERAL INFORMATION:
; APPLICANT: University of Leeds
; APPLICANT: Markham, Alexander F.
; APPLICANT: Jackson, Andrew P.
; APPLICANT: Woods, Christopher G.
; TITLE OF INVENTION: Treatment of Cancer and Neurological Diseases
; FILE REFERENCE: 9052-144
; CURRENT APPLICATION NUMBER: US/10/276,934
; CURRENT FILING DATE: 2002-11-20
; PRIOR APPLICATION NUMBER: PCT/GB01/02240
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: GB0012186.3
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent version 3.1
; SEQ ID NO 2
; LENGTH: 6145
; TYPE: DNA

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; LOCATION: (388)..(588)
; OTHER INFORMATION: "n" is any nucleotide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (624)..(624)
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; LOCATION: (672)..(672)
; OTHER INFORMATION: "n" is any nucleotide
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; LOCATION: (2265)..(2265)
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; LOCATION: (5468)..(5468)
; OTHER INFORMATION: "n" is any nucleotide
; NAME/KEY: misc feature
; LOCATION: (6027)..(6027)
; OTHER INFORMATION: "n" is any nucleotide
US-10-276-934-2

Alignment Scores:
Pred. No.: 0
Score: 6391.00
Percent Similarity: 80.90%
Best Local Similarity: 66.83%
Query Match: 41.16%
DB: 15
Matches: 6145
Conservative: 260
Mismatch: 278
Indels: 75
Gaps: 7

US-10-016-248-2 (1-3104) x US-10-276-934-2 (1-6145)
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Db      66 GTGAAAGGCGCATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCG
Qy      56 SerGlnLYeThrSerVal-----
Db      126 ACCCAATAAACTCTGTCTGCGATTCGATTCGATTCGATTCGATTCGATTCGATTCG
Qy      62 -----
Db      186 TAGCTTCAATATGATCTCGGAAACCATGCGCTTCAGAAATTCAGATGAGCCAGAG
Qy      70 Y-----
Db      246 AGGTGTGATTCGCTCTGACATGTCCTGATTCGATTCGATTCGATTCGATTCGATTCG
Qy      85 gLeuGlySerAspPheArgLeuGlySerSerValGlnPheThrCyseGlnGlyTYrAs 105
Db      306 ACCAGGTTCCGACTTCAGGGTTGGTGAATGTAAGTTTCATGTCGATTCGATTCGATTCG
Qy      105 sLeuGlnGlySerIysArgIleThrCyseMetIysIserAspMetPheAlaIleTyrSe 125
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Qy      125 rAspHisArgProValCYsArgAlaArgMetCyseAspAlaHisIleLeuArgGlyProSerG 145
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Qy      165 eIleThrAlaLeuAsnProSerIysValIleIysLeuAlaPheGluGluPheAspLeuG 185
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[illegible]

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Db	1638	GACAGAGGTCAATTATGACACCTTGAGAGTCAAGATGAGGCGACGAGTTGGTCCCACT	169
Qy	577	uILEGIyValTYrHisGLYThrGlnValProGlnPheLeuILESerThrSerAsnTYrLe	597
Db	1698	GATCGGCAGATACCCGCGACCCGAGCCAGTTCCTCATACGACCGGGAACCTTCAT	175
Qy	597	uTYrLeuLeuPheSerThrAspLYrSerHisSerAspRILeGIyPheGlnLeuArgTYrGI	617
Db	1758	GTACCTGGTATATCACCACTGACACACGCGCTCCAGCATCGGCTTCTCATCTCACTAAGA	181
Qy	617	uTHRLeuThrLeuGlnSerAspPHILeCYLeuAspProGIyLLeProValAsnGIyGlnAr	637
Db	1818	GAGTGTGACGCTTGAGTGGATTCTCGCTGGACCCGGGCAATCCTGTGAACGGCATTGG	187
Qy	637	GHILEGIyAsnAspPheTYrValGIyAlaLeuValThrPheSerCYAspAspSerGIyTYrTh	657
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Qy	657	rLeuSerAspGIyGIuProLeuGluCYGluProAsnHegINTPrSerArGIAlaLeuPr	677
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Db	1998	CAGCTGCACACGCTCTATGTGAGAGCTCATTCACAGGAAGATGGAACAGTCTTCTTC	205
Qy	697	oGIyPheProAspPheTYrProAsnAsnLeuAsnCYArThrTRIleIIeGIuThrSerHI	717
Db	2058	TGGGTTTCCAAATTTTATCCAACTCTCTAACTGCACAGTGACATTTGAAGTCTCA	211
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Db	2118	TGGGAAGAGATCAAAATGATCTTTCACACCTTTCATCTTGAAGATCCACAGACTATT	217
Qy	737	uLeuILEThrGluAsnGIySerPheThrGlnProLeuArgGlnLeuThrGIySerArgLe	757
Db	2178	ACTGATTCACAGAGATGGAAGTTTTCGCAAGCCGCTGCCAGGCTCACCGGGTGGTGT	223
Qy	757	uProAlaProIIeSerAlaGIyLeuTYrGIyAsnPheThrAlaGlnValArGpHeIIeSe	777
Db	2238	GCCTCATATGATCAAGGACGCGTGTGGAACCTTCACCTGCCAGCTTCGGTTATATATC	229
Qy	777	rAspPheSerMetSerTYrGIuGIyPheAsnIIeThrPheSerGIuTYrAspLeuGluPr	797
Db	2298	AGACTTCTCAATTTCTGTCAGAGGGCTTCAAATATCATTTTCAGAAATATGACCTGGACC	235
Qy	797	oCYeGIuLupProGluValIProAlaTYrSerIIeArgyegLYLeuGlnPheGIIyValGI	817
Db	2358	ATGTGATATATCTGGAAGTCCCTGCCCTTACGCGAAGAAATGGTTTTCATTGGGTGGG	241
Qy	817	yAspThrLeuThrPheSerCYsPheProGIyTYrArGLeuGluGIyThrAlaArgIIeTh	837
Db	2418	AGACTCTGACGTTTCTCTGCTTCCTGGATATGTTTAGAAGGTGCCACCAACCTTAC	247
Qy	837	rCYsLeuGIyGIyArGArGArGLeuTIPrSerSerProLeuProArgCYeValAlaGIuCY	857
Db	2478	CTGCTCGGTGGGGGGCCGCGTGTGAGTGAAGTCACTCTGCCAAGTGTGAGCGGAATG	253
Qy	857	egLYAsnSerValThrGIyThrGlnGIyThrLeuLeuSerProAsnPheProValAsnTY	877
Db	2538	TGAGCAAGTGTCAAAGGAATGAAGGAACATTACTGTCTCCAAATTTTCCATCCATTA	259
Qy	877	rAsnAsnAsnHisGIuCYsIIeTYrSerIIeGlnThrGlnProGIyLYyegLYIleGlnLe	897
Db	2598	TGATATATTAACCATGAGTGTATCTATAAATGAACAACAAGCGCGCAAGGCGATCACCT	265
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RESULT 9

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US-10-276-934-4
; Sequence 4, Application US/10276934
; Publication No. US20030180750A1
; GENERAL INFORMATION:
; APPLICANT: University of Leeds
; APPLICANT: Markham, Alexander F.
; APPLICANT: Jackson, Andrew P.
; APPLICANT: Woods, Christopher G.
; TITLE OF INVENTION: Treatment of Cancer and Neurological Diseases
; FILE REFERENCE: 9052-144
; CURRENT APPLICATION NUMBER: US/10/276,934
; CURRENT FILING DATE: 2002-11-20
; PRIOR APPLICATION NUMBER: PCT/GB01/02240
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: GB002186.3
; PRIOR FILING DATE: 2000-05-20
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent version 3.1
; SEQ ID NO 4
; LENGTH: 5667
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: misc_feature
; LOCATION: (588)..(588)
; OTHER INFORMATION: "n" is any nucleotide
; FEATURE:
; NAME/KEY: misc_feature

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; LOCATION: (2265)..(2265)
; OTHER INFORMATION: "n" is any nucleotide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5641)..(5641)
; OTHER INFORMATION: "n" is any nucleotide
US-10-276-934-4

Alignment Scores:
Pred. No.: 0
Score: 6978.00
Percent Similarity: 81.12%
Best Local Similarity: 67.03%
Query Match: 41.08%
DB: 15
Gaps: 7

US-10-016-248-2 (1-3104) x US-10-276-934-4 (1-5667)

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Qy 56 SerGlnLysThrSerVal 61
Db 126 AGCCATMAAACTGTGCTGCGCATATGAAATTAACATACCATGTGATCCAGACAGA 185
Qy 62 -----LeuThrGln-ValGlyValSerGlnG 70
Db 186 TAGCTTATTATGATCTGGGAAACCATGCTTCAAGTAAATTCAGTGAAGCCAAAG 245
Qy 70 y-----HisAsnMetCysProAspProGlyIleProGluArgGlybAr 85
Db 246 AGGTGTTCATTTGCTGTCATGATGTCATGATGTCATGATGTCATGATGTCATGATG 305
Qy 85 gLeuGlySerAspPheArgPheArgLeuGlySerSerValGlnPheThrCysAsnGlyIlyrAs 105
Db 306 AGCAGGTTCCGACTTCCAGGCTGCTGCAATGTCATGATGTCATGATGTCATGATG 365
Qy 105 pLeuGlnGlySerLysArgIleThrCysMetLysValSerAspMetPheAlaIatPse 125
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Qy 277 nGlySerCyGlyAaPProGlyIleProAlaTyGlyAArgGluGlySerAArgPheH 297
Db 798 GGGAGGGGTGGGATCTGGAAATCCCGCTATGGGAAGGAGCGGAGCACTTTCTCT 857
Qy 297 sHieGlyAaPThrLeuIyPheGluCyGlnProAlaPheGluLeuValGlyGlnIySaI 317
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QY	1697	YTYRLALEUNGNGLYNH1EALAH1E1SESCYMERPROGJLYTHRVALLARGATTPAS	1717
DB	5058	GFACACCTGCGAGGGCCGGTCCCAATTTCCTGATGCCAGGACCGTTGGCGGSA	5117
QY	1717	NTYRPROBROPROLEUCYSIIIEALG1NCYSGLYGLYTHRVALLG1UG1METGLUGLYVA	1737
DB	5118	CTATCCGCTCCCTCCGTGCATTTGCACCACTGTGTGAGGAGCGCTGAGCACTTGGGGTGGT	5177
QY	1737	IIIEUSERPROGJLYRHEPROGJLYANTRYRPROSERSEMELAPYSSERTPLVSI	1757
DB	5178	GATCCCTGAGCCCCGGGCTTCCAGAGTTCCTTACCCCAACAACCTTAGCTGCACCTGAGAGT	5237
QY	1757	EALAEUPROYALG1YPHAGLYVALAH1E1GL1NPH1EUA5NPHE5ERTHGIUPROAS	1777
DB	5238	CTCATTACCACATCCGCTATGTCGACACATTTTCAGTTTCTGAATTTTCTTACCGAAGCTRA	5297
QY	1777	NH1EAPTRY1LEG1U1EARGANGLYPROTYG1LUTH1R5ERAGMETG1YARGPH	1797
DB	5298	TCATGACTCTCCCTGAAATTCAAATGAGCACTTACACACGACCCCATGATTTGACAT	5357
QY	1797	ESEGLYSERLIUEUPROSERSELEULEN5ERTH5ER1EG1UTH1RVALTYRPH	1817
DB	5358	TAGCGGCGAGGATCTCCCGGGCGGCTGTGACGACCAAGCATGAAACCTTCATCCACT	5417
QY	1817	EH1SE5ERAPH1IS5ERG1NA5NARGYPROGJLYPHELY5EUG1LUTYRG1NALA	1834
DB	5418	TTATATGATACCATTCGCAAAACCGGCAAGATTTTAACTTCTTACCAAGCC	5469
RESULT 10			
US-10-467-042-27			
Sequence 27, Application US/10467042			
Publication No. US20040077048A1			
GENERAL INFORMATION:			
APPLICANT: WARREN, Bridget A.; HONGHELL, Cynthia D.;			
APPLICANT: LU, Yan; CHAWLA, Nandinder K.;			
APPLICANT: BURFORD, Neil; DELESEANE, Angelo M.;			
APPLICANT: GANDHI, Ameena R.; BAUGHN, Mariah R.;			
APPLICANT: GRIFFIN, Jennifer A.; GIERZEN, Kimberly J.;			
APPLICANT: LU, Dying Aina M.; ISON, Craig H.;			
APPLICANT: RAMKUMAR, Javalaxmi; TANG, Y. Tom;			
APPLICANT: LAU, Preeti G.; BOROWSKI, Mark L.;			
APPLICANT: DUGGAN, Brendan M.; HARPLA, April J.A.;			
APPLICANT: ARVIZU, Chandra S.; THANGAVELU, Kavitha;			
APPLICANT: YAO, Montique G.; ELLIOTT, Vicki S.;			
APPLICANT: DING, Li; YUE, Henry;			
APPLICANT: LEE, Sally; SWARNAKAR, Anita;			
APPLICANT: TRAN, Uyen K.; XU, Yuming			
TITLE OF INVENTION: PROTEIN MODIFICATION AND MAINTENANCE MOLECULES			
FILE REFERENCE: PI-0361 USN			
CURRENT APPLICATION NUMBER: US/10/467,042			
CURRENT FILING DATE: 2003-07-31			
PRIOR APPLICATION NUMBER: PCT/US02/02813			
PRIOR FILING DATE: 2002-01-30			
PRIOR APPLICATION NUMBER: US 60/265,705			
PRIOR FILING DATE: 2001-01-31			
PRIOR APPLICATION NUMBER: US 60/266,762			
PRIOR FILING DATE: 2001-02-05			
PRIOR APPLICATION NUMBER: US 60/269,581			
PRIOR FILING DATE: 2001-02-16			
PRIOR APPLICATION NUMBER: US 60/271,198			
PRIOR FILING DATE: 2001-02-23			
PRIOR APPLICATION NUMBER: US 60/272,813			
PRIOR FILING DATE: 2001-03-01			
PRIOR APPLICATION NUMBER: US 60/275,586			
PRIOR FILING DATE: 2001-03-13			
PRIOR APPLICATION NUMBER: US 60/278,505			
PRIOR FILING DATE: 2001-03-23			
PRIOR APPLICATION NUMBER: US 60/280,539			
PRIOR FILING DATE: 2001-03-30			
NUMBER OF SEQ ID NOS: 32			
SOFTWARE: PERL Program			
SEQ ID NO 27			

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/ LENGTH: 4506
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ OTHER INFORMATION: Incyte ID No: 7473634CB1
US-10-467-042-27

Alignment Scores:
Pred. No.: 0 Length: 4506
Score: 4148.50 Matches: 775
Percent Similarity: 71.53% Conservative: 190
Best Local Similarity: 57.45% Mismatches: 255
Query Match: 24.42% Indels: 119
DB: 16 Gaps: 15

US-10-016-248-2 (1-3104) x US-10-467-042-27 (1-4506)
QY 1 MetalagiYalAProProProAlaLeu-----LeuProCySerLeu 15
DB 385 ATCAATGGACGACGAAGCTTCATCCATATGAGCTAACTGCATGAACCTCCCTCCAGTT 444
QY 16 IleserAap-----CyCyAlaSerAsnGlnaGhIleser 27
DB 445 ATCAATGACGAAGAATTGGCTACGACTCCATTCACTCTGACAGCAACACGACGAAA 504
QY 28 ValgiYalgiYProSerGlnuValiYlsYsGlnIleGluLeuYsSeragiYal 47
DB 505 ---GGATTAAAGCTCAGTTCCAAGTGAAGAAAGGCGATTGAGTTGAAGTCAGAGAGATC 561
QY 48 LysleuMetProSerLysAspAsnSerGlnYsThrSerValLeuThrGlnValgiYal 67
DB 552 AAGATGCTGCGCCACGACGAAGATGAAGAACCATMAAACTCTGCTTGAAGCAGAGGT 621
QY 68 SerGlnGlnYHsasMetCyAProAspProGlyIleProGlnaYalgiYlsarGleuGly 87
DB 622 GCATTGCTCTCGACATGTCTCCAGATCTCTGGATTCCAGAAATGTGTAAGACAGAT 681
QY 88 SerAspPhearGleuGlySerSerValGlnPheThrCyAsnGlnGlyTyrrAspleuGln 107
DB 682 TCCGACCTTCAGGGTGTGTCGCAAAATGTACAGTTTCATGTGAGAGACATAACGTGCTCCAG 741
QY 108 GlySerLysAspGlieThCyMetLysValSerAspMetPheAlaIleThrSerAspHis 127
DB 742 GAATCTTAAGCATCACTGTCAGAGATTCACAGAGCGCTCGCTGTGGATGCCAC 801
QY 128 ArgProValCySarGlnaArgMetCyAspAlaHisLeuArgGlyProSerGlyIleIle 147
DB 802 AGGCCCATCTCGCGACGAGAACATGTGATCAATCTGCGTGGGGCCAGCGGCGTCATT 861
QY 148 ThrSerProAsnPheProIleGlnTyrrAspAsnAlaHisCyValaTrpIleIleThr 167
DB 862 ACCCTCCCTTAATTATCCGTTCAAGTATAAAGATATATGACACTGTGTGTGGGTCACTACC 921
QY 168 AlaLeuAsnProSerLysValIleYsLeuAlaPheGlnGlnPheAspLeuGlnArgGly 187
DB 922 ACCACCAACCCGACAGAGTCAATCAAGCTTGCTTTGAAGACTTTGAGCTGACGACGAC 981
QY 188 TyrrAspThrLeuThrValgiYasPgiYlGlnaPgiYasPgiYasPgiYasPgiYasPgiYas 207
DB 982 TATACACACCCGACGGTGTGATGCTGGAGAGCGGAGACACACAGATCGGTCTTGTAC 104
QY 208 MetSerGlnaAlaCySerAspSerProHisThrProGlySerArgIleProGlu--- 226
DB 1042 GTG-----CTCAGCGGATCCAGTGTCTTCACTC 1077
QY 227 -----SerMetSerGlyAspIleThrArgGlnYsTrpThrValLeuGlnIleCySarG 244
DB 1072 ATTGTGAGCATAGACACACCAAGATGTGCTAAT----- 110
QY 245 AspIleSerSerSerAspAlaArgSerGlySerValaArgLysSerProLysThrSerAsn 264
DB 1105 ---CTGCAAGTCGATGATAGC----- 1122

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QY	265	AlaValGluLeuValAlaProGly-----ThrGluIleGluGlnGlySer	279
Db	1123	-----ATTGGCTCACTGGGGTTTAAAGCTGTTTACCAAGAAATTGAAAGGAGGCG	1173
QY	280	CysGluAerProGlyIleProAlaTyrglyArgArgGluGlySerArgPheHisIleGly	299
Db	1174	TGTGGGGATCTCGGAATCCCGCCCTATGGGAAGCGGACGGGACGAGATTCTCTCATGGA	1233
QY	300	AspThrIleuLysPheGluCysGlnProAlaPheGluLeuValGlyIleValAlaIleThr	319
Db	1234	GATACACTCACCTTGGAAATGCCCGGCGCTTTGAGCTGTGGGGGAGAGATTATCACCC	1293
QY	320	CysGlnLysAerAerGlnTrpSerAlaLysLysProGlyCysValPheSerCysPhePhe	339
Db	1294	TGTCAAGCAACAACTACGTGGCTCTGGCAACAGCCACACTGTGTATTTTCAATGTTTCTTC	1353
QY	340	AsnPheTrpSerProSerGlyValValLeuSerProAerTrpProGluAerDyrglyLys	359
Db	1354	AACCTTACGGCATCATCTGGGATTATTTCTGCACCAAAATTATCCAGAGAAATATGGGAC	1413
QY	360	HisLeuHisCysValTrpLeuIleLeuAlaArgProGluSerArgIleHisLeuAlaPhe	379
Db	1414	AACATGAACTGTGTCTGGTATTATTCGAGAGCCAGGAAGTCGAATTCACCTAATCTTT	1473
QY	380	AsnAspIleAerPvalGluProGlnPheAerPheLeuValIleLysAerGlyAlaThrAla	399
Db	1474	AATGATTTTGTATGTTGAGCCCTCAATTTGACTTTCGCGGCAAGATGATGGCATTTCT	1533
QY	400	GluAlaProValIleuGlyThrPheSerGlyAerGlnLeuProSerSerIleThrSerSer	419
Db	1534	GACATATCTGCTCGGTACTTTTCTGGCAATGAAGTCCTTCCAGCTGGACCGACAGCT	1593
QY	420	GlyHisValAlaArgLeuGlnPheGlnThrAspHisSerThrGlyLysArgGlyPheAsn	439
Db	1594	GCGCATATAGTTCCTGTGGAATTCAGTCTGACACTTCACATCTGCGAGAGGGTTCAAC	1653
QY	440	IleThrPheThrThrPheArgHisAsnGluCysProAerProGlyValProValAsnGly	459
Db	1654	ATCATCTTACCAACCATTTGGTCAGAAATGATGCCATGTATCTCGGCAATTCCTATTAACGA	1713
QY	460	LysArgPheGlyAerSerLeuGlnLeuGlySerSerIleSerPheLeuCysAerGluGly	479
Db	1714	CGACGTTTGGTGAACAGGTTTCTATCTGGGAGCTCGGTTTCTTTCACCTGATGATGCGC	1773
QY	480	PheLeuGlyThrGlnGlySerGluThrThrIleThrCysValLeuLysGluGlySerValVal	499
Db	1774	TTTGTCAAGACCCAGGAGATCCGAGTCCATTACTGCAATGCAAGAGGGAAACGTGGTTC	1833
QY	500	TrpAsnSerAlaValLeuArgCysGluAlaProCysGlyGlyHisIleuThrSerProSer	519
Db	1834	TGGAGCTCCACCGTCCCGCGCTGTAACTCCATGTGGTGAACATCTGACAGCGTCCAGC	1893
QY	520	GlyThrIleLeuSerProGlyTrpProGlyPheTyryLysAerAlaLeuSerCysAlaTrp	539
Db	1894	GGAGCATTTTGCCCTCGTGAATGGCAGAAATATTAAGATTTCTTTACATTGTAATGG	1953
QY	540	ValIleGluAlaGlnProGlyTyryrProIleLysIleThrPheAerArgPheLysThrGlu	559
Db	1954	ATAATGTGAAGCAAAACAGGCCCATCTGTACAAATAACTTTTGTGACAGATTTCAACAGAG	2013
QY	560	ValAsnTyryrAerThrLeuGluValAlaArgAerGlyArgThrTyryrSerAlaProLeuIleGly	579
Db	2014	GTCATATTGACACTTGGAGGTCAAGATGGGCCAGCAAGTGTCTCCCATGTATGGGC	2073
QY	580	ValTyryHisGlyThrGlnValProGlnPheLeuIleSerThrSerAsnTyryrLeuTyren	599
Db	2074	GAGTACCAAGGCAACCCAGGCAACCCAGATTCTCATCAACACCGGAACTTCATGATCACTG	2133
QY	600	LeuPheSerThrAspLysSerHisSerAspIleGlyPheGlnLeuAlaGlytyrGluThrIle	619
Db	2134	CTGTTTACACCTGACACAGCCGCTCCAGCATGGCTTCTCATCATCACTATGAAGATGTG	2193

QY	620	ThrLeuGlnSerAspHisLeuValLeuAspProGlyLysProValAsnGlyValAsnHisGly	639
Db	2194	ACGGTATGTCGATTCCTGCTGTGACCCGGGACCTCTGGAAAGGCATCGCCAGGT	2253
QY	640	AsnAspPheTyrValGlyAlaLeuValThrPheSerCysAspSerGlyTyrThrLeuSer	659
Db	2254	GGAGACTTGGGCATCAGGTCCACAGTGAATCTTACGCTGTACCCGGGGTACACCTAAGT	2313
QY	660	AspGlyLysProLeuGlnCysGlyLysProAsnPheGlnTrpSerArgAlaLeuProSerCys	679
Db	2314	GACGACGAGCCCTCGTCTGTGAGAGAAACCAACAGTGAACCAACGCGCTTGCCAGCTGC	2373
QY	680	GluAlaLeuCysGlyGlyPheIleGlnGlySerSerGlyThrIleLeuSerProGlyPhe	699
Db	2374	GACGCTCATGTGAGGCGTACATCCAAAGGGAAGTGGAAACAGTCTTTCTCCGGGTTT	2433
QY	700	ProAspPheTyrProAsnAsnLeuAsnCysThrTrpIleIleGlnTrpSerHisGlyLys	719
Db	2434	CCAGATTTTATCCAAATCTCTTAACTGCACGTGGACCATTTGAAGTGTCTCATGGAAA	2493
QY	720	GlyValPhePheThrPheHisThrPheHisLeuGlnSerGlyHisAspTyrLeuLeuIle	739
Db	2494	GGAGTCAAATGATCTTTCACACTTTTCATCTTGAGATTGCCACGACTATTATCTGATC	2553
QY	740	ThrGluAsnGlySerPheThrGlnProLeuArgGlnLeuThrGlySerArgLeuProAla	759
Db	2554	ACAAGAGGTGAAATTTTTCGACCCGCTCCAGCTCCACGGGTGCGTGTGCTTCAT	2613
QY	760	ProIleSerAlaGlyLeuTyrGlyAsnPheThrAlaGlnValArgPheIleSerAspPhe	779
Db	2614	ACGATCAAAGGAGGCGCTGTGGAACTTCCATCGCCAGCTCGTGTATATATACAGCTTC	2673
QY	780	SerMetSerTyrGlnGlyPheAsnIleThrPheSerGlnTyrAspLeuGlnProCysGlyL	799
Db	2674	TCATTTTCGTATCGAGGCGCTTCAATATACATTTTCABAATATAGACTGGAGCATGTGAT	2733
QY	800	GluProGluValProAlaTyrSerIleArgLysGlyLeuGlnPheGlyValGlyAspThr	819
Db	2734	GATCTCGAGAGCCCTGCGCTTCAGCCGAAATGTTGTTTTCATTTGGTGTGGAGACTCT	2793
QY	820	LeuThrPheSerCysPheProGlyTyrArgLeuGlnGlyThrAlaArgIleThrCysLeu	839
Db	2794	CTGACGTTTCTCTCTCTCTGGGATATCGTTTAAAGGTGCCACCAAGCTTACTGCTGTG	2853
QY	840	GlyGlyLysArgArgLeuTyrPheSerProLeuProArgCysValAlaGluCysGlyAsn	859
Db	2854	GCTGGGGGCGCCCGCTGTGTGAGAGCACCTCTGCAGAGCTGTGTGGCCGATGTGGAGCA	2913
QY	860	SerValThrGlyThrGlnGlyThrLeuLeuSerProAsnPheProValAsnTyrAsnAsn	879
Db	2914	AGTGTCAAAGGAATTAAGAAACATTAATCTGCTCAAAATTTTCCATTCATTAATATAT	2973
QY	880	AsnHisGluCysIleTyrSerIleGlnThrGlnProGlyLysGlyIleGlnLeuLysAla	899
Db	2974	AACCATAGGTATCTTAAATTAAGAAACGAAGCCGCGAAGGGCATCCACTTAGACA	3033
QY	900	ArgAlaPheGlnLeuSerGlnGlyAspValLeuLysValTyrAspGlyAsnAsnAsnSer	919
Db	3034	CGAAGCTTCCAGCTGTGTAAGAGATACCTTAAAGGTATATGTAAGAAAAGACAGTCC	3093
QY	920	AlaArgLeuLeuGlyValPheSerHisSerGlnMetMetGlyValThrIleAsnSerThr	939
Db	3094	TCACGTCCACGTGGCAGCTTCACTAAATTAAGAACTTGGGGGCTGATCTTAAACAGACA	3153
QY	940	SerSerSerLeuTrpLeuAspPheIleThrAspAlaGluAsnThrSerLysGlyPheGln	959
Db	3154	TCCATATCACCTGTGGCTAAGGTTCAACACCAATGATCTACACACGCAAGGTATTGCA	3213
QY	960	LeuHisPheSerSerPheGlnLeuIleLysCysGlnAspProGlyThrProLysPheGly	979
Db	3214	CTACACTATACGATTTTGATCTGTGTAAATGTGAGGATCCGGGACATCCTTAATACGCG	3273
QY	980	TyrTyrValHisAspGlnGlyHisAspHisGlySerSerValSerPheSerCysAspPro	999


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; PRIOR APPLICATION NUMBER: US 60/255,622
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PERL Program
; SEQ ID NO 31
; LENGTH: 2609
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 747363OCB1
US-10-399-455-31

Alignment Scores:
Pred. No.: 4.4e-238 Length: 2609
Score: 2694.00 Matches: 493
Percent Similarity: 73.17% Conservative: 126
Best Local Similarity: 58.27% Mismatches: 175
Query Match: 15.86% Indels: 54
DB: Gaps: 4

US-10-016-248-2 (1-3104) x US-10-399-455-31 (1-2609)

QY 887 IleglnThrGlnProGlyLysGlyIleglnLeuLysAlaArgAlaPheGlnLeuSerGln 906
DB 124 GTCCAGGAGCTCCCAATCAGGAAATCATCTGACTCCAAAGGAGGAGAG-----CAG 177
QY 907 GlysPheValLeuLysValIleAspGlyAspAsnAsnSerAlaArgLeuLeuGlyValPhe 926
DB 178 GGCACAGATGGC-AGGATTATGATGAGAAAGATAAAGCATCATCTAATAGGTGCTTTT 236
QY 927 SerHisSerGlnMetGlyValThrLeuAsnSerThrSerSerSerLeuThrPheAsp 946
DB 237 ACTGGTCATCTATGCGCGAGCTGACACTAGTAGTCTTCAATCAACTCTGGCTAGAA 296
QY 947 PheIleThrAspAlaGlnAsnThrSerLysGlyPheGlnLeu----- 960
DB 297 TTTAAATCCGATACTGAAGGAGCAGATGAAGGCTTTCACTGTGTATACCAAGAGATTC 356
QY 960 ----- 960
DB 357 ATAGGATTTGCAGAGAGGTCAACAGTCTACATTCAGACAAATCAGAACAGGACGAGAA 416
QY 961 -----HisPheSerSerPheGlnLeuIleLysCysGlnAspProGlyThrPro 976
DB 417 CATTTGCTAGGAGAGAG-TCAGGTTTGAATCTGCACACTGTGAAGTCTCTGGCATTTCA 475
QY 977 LysPheGlyLysLysValHisAspGlnGlyHisPheAlaGlySerSerValSerPheSer 996
DB 476 CAATTGGATACAAAGATCAGTGAACCAAGGCCACTTGTGGTAGCACCAATCATTTATGGA 535
QY 997 CysAspProGlyLysSerLeuAspGlyLysSerGlnGlyLeuLeuLysCysLeuSerGlyLysArg 1016
DB 536 TGCATTCACAGGCTCACTCCACGAGAGT----- 565
QY 1017 ArgThrTrpAspArgProLeuProThrCysVal-AlaGlnCysGlyGlyThrValArgGln 1036
DB 566 -----AGCCTTCTCAACGATGAGAGTGGAGGTGGTTTAAAG 601
QY 1036 YgiValSerGlyGlnValLeuSerProGlyLysProAlaProTyrGlnHisAsnLeuAs 1056
DB 602 AGAATCATCTACGAGAAATCTTATCTCTGGCTATCTCTTCCATATGACAAATAACTGGG 661
QY 1056 nCysIleTrpThrIleGlnAlaGlnLysCysThrIleGlyLeuHisPheLeuValPhe 1076
DB 662 TTGCATGTGGATGATTGAGGTAGATCCTGGAAATATTCAGCTTGCAGTTCTTCTGCTTT 721
QY 1076 eAspTrpGlnGlnValHisAspValLeuArgIleTrpAspGlyProValGlnSerGlyVal 1096
DB 722 TGATAGGAGAGCATCAATGATATCTCGAGCTGGAGCGGTCCACGAAATATGATAT 781
QY 1096 IleuLeuLysGlnLeuSerGlyProAlaLeuProLysAspLeuHisSerThrPheAsnSe 1116
DB 1116 -----

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DB 782 GCTTTAAAGAAATTAGTGATCTTTATTTCTGAGAGAAATTCATAGCACTCAATAT 841
QY 1116 rValValLeuGlnPheSerThrAspPheThrSerLysGlnGlyPheAlaIleGlnPhe 1136
DB 842 AGTAACCATTCAGATTGACACGAGATTTTATATAGCAAAATCGATTGGCAATTCAGTT 901
QY 1136 eSerValSerThrAlaThrSerCysAsnAspProGlyIleProGlnAsnGlySerArgSe 1156
DB 902 TTCAAGTCTGTGGCCACTGCGGTGCTGATCCAGGAGGTCCCATGAAATGGAGCTCGAAA 961
QY 1156 rGlyAspSerTrpGlnAlaGlyAspSerThrValPheGlnCysAspProGlyLysValLe 1176
DB 962 TGGGATGAGAGAGAACTGGGAGACACTGTTGTTTTCATATGATGACCCAGATATAACT 1021
QY 1176 uGlnGlySerAlaGlnIleSerCysValLysIleGlnAsnArgPhePheTrpGlnProSe 1196
DB 1022 TCAGAGAGAGAGAAAGAAATACCTGATTCAGATGAGAAATCGGTACTTGGCAGCGCCAG 1081
QY 1196 rProProThrCysIleAlaProCysGlyLysAspLeuThrGlyProSerGlyValIleLe 1216
DB 1082 CCACACAGTCTGTATAGCACCTGTGAGGCAATTTAACAGGATCTTCAGGCTTTATTTCT 1141
QY 1216 uSerProAsnTrpProGlnProTyrProProGlyLysGlnCysAspTrpLysValThrVal 1236
DB 1142 TTCACCAAACTTCCCTCATTCATATCCGATAGCAGAGCTGTGACTGACTATCACCT 1201
QY 1236 lSerProAspTrpValIleAlaLeuValPheAsnIlePheAsnLeuGlnProGlyLys 1256
DB 1202 CAATGACAGCTATGTATCTCTCTGCGCTTCATCAGTTTATGACATAGAACCAACTATGA 1261
QY 1256 PheLeuHisIleLysIleAspGlyValArgAspSerLeuSerProLeuIleGlySerPheThrGln 1276
DB 1262 CTTCCTCTATATCTATGATGACCCAGACATATAGCCCACTGATGAGTTTCAMAGA 1321
QY 1276 YSerGlnLeuProGlyArgIleGlnSerSerSerAsnSerLeuPheLeuAlaPheArgSe 1296
DB 1322 CAGCAAGATTACAGAGAGAAATGAGAACGACTCAATATCAATGATTCATTCGCTTTGGAG 1381
QY 1296 rAspAlaSerValSerAsnAlaGlyPheValIleAspTrpThrGlnAsnProArgGlnSe 1316
DB 1382 TGATGATCTGTATATTACACTGATTCATCTTAAATACAAAGCAAACTGCGAGAGTC 1441
QY 1316 rCysPheAspProGlySerIleLysAsnGlyThrArgValGlySerAspLeuLysLeuGln 1336
DB 1442 CTGCTTATATCCAGCAATATATGAAATGCAACCACTTGGATGAGATTATTAATTGAG 1501
QY 1336 YSerSerValThrTrpCysHisGlyLysGlyLysGlnGlyLysThrSerThrLeuSe 1356
DB 1502 GTCAACAGTCACTATTTACTGTGATGCTGGTTATGTTCTTCAAGGTTATTTCAACACTCAC 1561
QY 1356 rCysIleLeuGlnProAspGlyLysProValThrAsnAsnProArgProValCysThrAl 1376
DB 1562 CTGTTTCAATGGAGATGATGAGAGACCTGAGTGAATGAGACCTTGGCAAGTTGTCATGC 1621
QY 1376 aProCysGlyLysGlnTrpValGlySerAspGlyValValLeuSerProAsnTrpProGln 1396
DB 1622 GCCCTGTGAGAGTGTTCACAGGTTCAAGAGGACGCTTTATATCACCAAACTATCCAA 1681
QY 1396 nAsnTrpThrSerGlyGlnIleCysLeuTrpPheValThrValProLysAspTrpValVal 1416
DB 1682 AAATTAACGTGGAGACATAATGTGTATTTATTCATAGACGTTCCAAAGGAGTGTGGTG 1741
QY 1416 lPheGlyGlnPheAlaPhePheHisThrAlaLeuAsnAspValValGlnValHisAspGln 1436
DB 1742 TTGG---CCAAGTTATTTTTCACAGACATCTCACAGATGTTTGAAGTGTATGAGG 1798
QY 1436 YHisSerGlnHisSerArgLeuLeuSerSerLeuSerGlySerHisThrGlyLysSerLe 1456
DB 1799 GCCAACTCAGCAATCTTCTGTATCTTCCTCTTCAGATCCCATTCAGAGAGATCACT 1858
QY 1456 uProLeuAlaThrSerArgGlnValLeuIleLysPheSerAlaLysGlyLeuAlaProAl 1476
DB 1859 TTCACAGTTCAGGTATACGATGACAAATTCGATTTCACTGAGTGGACCAATATACAGC 1918

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Qy 1476 aArgGlyPheHisPheValTyrGlnAlaValProArgThrSerAlaThrGlnCysSerSe 1496
Db 1319 TAAGGATTTTCACTTTGTTTACCAAGCTGTTCTTCAACCAAGTTTACCAATGCAGTTT 1978
Qy 1496 rValProGluProArgTyrGlyLysArgLeuGlySerAspPheSerValGlyAlaIleVa 1516
Db 1979 TGTCCTGTAACCAAGATTCGGAAGAAAGATTGGCAATGAATTTGGAGTCGGTTCATCGCT 2038
Qy 1516 lArgPheGluCysAsnSerGlyTyrAlaLeuGlnGlySerProGluIleGluCysLeuPr 1536
Db 2039 TCTTTTGATTTGATTCAGATATATTTCTCCATGATCCATAGCAATTTAGGTGTAAC 2098
Qy 1536 oValProGluValLeuAlaGlnTTPAsnValSerAlaProThrCysValAlaProCysG 1556
Db 2099 AGTCCCAATTTCTTTGGCCCAAGGATGATTCCTTACTTCTTGTATGTCCTGTTGG 2158
Qy 1556 yGlyAsnLeuThrGluArgArgGlyThrIleLeuSerProGlyPheProGluProTyrLe 1576
Db 2159 TGAATTTTAACTAAGCGCAAGGACTAATTTTGTCACTGGATACCTGAGCCTTATGA 2218
Qy 1576 uAsnSerLeuAsnCysValITTPyIleValAlaProGluGlyAlaGlyIleGlnIleG 1596
Db 2219 CAACAATCTGAATGTGTGTGGAAGATCACAGTGCAGAGGAGCTGCATTCAAGTCA 2278
Qy 1596 nValValSerPheValThrGluGlnAsnTTPAspSerLeuGluValPheAspGlyAlaAs 1616
Db 2279 AGTTGTTAGCTTTGCTTACAGAACATATTTGGATTTCTTGGACTTTTATGATGGGGAGA 2338
Qy 1616 pAsnThrValThrMetLeuGlySerPheSerGlyThrThrValProAlaLeuLeuAsnSe 1636
Db 2339 CAACAATGCTCCAGACTTGGAGACTTACAGAAACAACAATCCCATCTTTGAATAG 2398
Qy 1636 rThSerAsnGlnLeuTyrLeuHisPheTyrSerAspIleSerValSerAlaAlaGlyPh 1656
Db 2399 TACCTCAATATATCTGATCTTAATTTCAATACAGACATCAGTGTCTTCTCGCAGGATT 2458
Qy 1656 eHisLeuGlnTyrLysThrValGlyLeuSerSerCysProGluProAlaValProSerAs 1676
Db 2459 TCATCTTGATTAACACAGCAATTTGGTTGGATTTCTGCTTCAACCAATCTCTTAGAG 2518
Qy 1676 nGlyValLysThrGlyGluArgTyrLeuValAsnAspValValSerPheGlnCysGluPr 1696
Db 2519 TGAATTTAAATTTGGAAGACATATATGTTGAGATGTACTATCTTCACTGATGATCA 2578
Qy 1696 oGlyTyrAlaLeuGln 1701
Db 2579 AGGATATTCTCTCAG 2594

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RESULT 13

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US-10-398-037-69
; Sequence 69, Application US/10398037
; Publication No. US20040138414A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS; YUE, Henry;
; APPLICANT: TANG, Y. TOM; NGUYEN, Daniel B.;
; APPLICANT: YAO, Monique G.; XU, Yaming;
; APPLICANT: TRIBOULEY, Catherine M.; SANJANMALA, Madhusudan M.;
; APPLICANT: CHAWLA, Nalinder K.; BAUGHN, Mariah R.;
; APPLICANT: SAPPERSTEIN, Stephanie K.; LAL, Preeti G.;
; APPLICANT: THORNTON, Michael B.; GANDHI, Ameena R.;
; APPLICANT: RAMKUMAR, Jayalaxmi; ELLIOTT, Vicki S.;
; APPLICANT: ARVIZU, Chandra S.; THANGAVELU, Kavitha;
; APPLICANT: GRIEZEN, Kimberly J.; DING, Li;
; APPLICANT: AU-YOUNG, Janice K.; TRAN, Bao;
; APPLICANT: POLICKY, Jennifer L.; LEE, Sally;
; APPLICANT: LU, Dyrng Alina M.; BURFORD, Neil;
; APPLICANT: WARREN, Bridget A.; GURURAJAN, Rajagopal;
; APPLICANT: DUGGAN, Brendan M.; HONCHELL, Cynthia D.;
; APPLICANT: HARALIA, April J.A.
; TITLE OF INVENTION: SECRETED PROTEINS
; FILE REFERENCE: PI-0240 USN
; CURRENT APPLICATION NUMBER: US/10/398,037

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; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: PCT/US01/30042
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/242, 218
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/236, 869
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/239, 812
; PRIOR FILING DATE: 2000-10-11
; PRIOR APPLICATION NUMBER: US 60/240, 108
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: US 60/241, 282
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: PERL Program
; SEQ ID NO 69
; LENGTH: 2387
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 6813464CB1
US-10-398-037-69

Alignment Scores:
Pred. No.: 4,656-233 Length: 2387
Score: 2639.00 Matches: 498
Percent Similarity: 91.53% Conservative: 10
Best Local Similarity: 89.73% Mismatches: 19
Query Match: 15.54% Indels: 28
DB: 17 Gaps: 5

US-10-016-248-2 (1-3104) x US-10-398-037-69 (1-2387)
Qy 1 MetAlaGlyAlaProProProAlaLeuLeuProCysSerLeuIleSerAspCys 20
Db 1 ATGGCGGGCGGCCCTCCCGCCCTGCTGCTGCTTGCAGTTGATCTGAGTGGCT 60
Qy 21 AlAsernGlnAlaGHisSerValGlyValGlyProSerGluLeuValLysGlnIle 40
Db 61 GCTAGCAATCAGCACACTCCGTGGGCTGAGACCTCCGAGCTAGTCAAGAACCAATT 120
Qy 41 GluLeuLysSerArgGlyValValLysLeuMetProSerLysAspAsnSerGlnLysThrSer 60
Db 121 GAGTTGAAGTCTCAGAGTGTGAAGCTAGTCCAGCAAGCAACAGCAGACGCT 180
Qy 61 ValLeuThrGlnValGlyValSerGlnGlyHisAsnMetCysProAspProGlyIlePro 80
Db 181 GTGTTAATCTCAGGTGGTGTGTGTCCCAAGGACATATATGTGTCCAGACCTCGCATGCC 240
Qy 81 GluArgGlyLysArgLeuGlySerAspPheArgLeuGlySerSerValGlnPheThrCys 100
Db 241 GAAAGGGGCAAAAGACATAGGCTCCGATTTCAAGATTCACAGCTCCAGTTCCACTGC 300
Qy 101 AsnGlnGlyTyrAspLeuGlnGlySerLysArgIleThrCysMetLysValSerAspMet 120
Db 301 AACGAGGCTATATGCTTCGAAAGGTTCCAAAGGAGTACCTGTAAGAAAGTAGAGACATG 360
Qy 121 PheAlaIatTPSerAspHisArgProValCysArgAlaArgMetCysAspAlaHisLeu 140
Db 361 TTTCGGGCTGTGAGCGACACAGCCAGCTCCGAGACCCGCGCATGTGTGATGCCACTT 420
Qy 141 ArgGlyProSerGlyIleIleThrSerProAsnPheProIleGlnTyrAspAsnAla 160
Db 421 CGAGGCCCTCGGCGATCATCACCCTCCCAATTTCCCATTCAGTATGACCAACAATGCA 480
Qy 161 HisCysValITTPIleIleThrAlaLeuAsnProSerLysValIleLysAlaPheGlu 180
Db 481 CACTGTGTGATCATCAACAGCACTAACCCCTCCAAAGGATCAAGCTGCTTGAG 540
Qy 181 GluPheAspLeuGluArgGlyTyrAspThrLeuThrValGlyAspGlyGlnAspGly 200
Db 541 GAGTTTATTTGAGAGAGGCTATGACACCTTGAACGCTGATGTGTGATGAGATGG 600

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1661 ----- 1661
Db 181 TAGGAAACCTGCTGCATACCTGGGAGCTGCTGCCCTACCCCTTTCTCCACTGGGATACAG 240
Qy 1662 -----ThrValGlyLeuSerSerCysProGluProAlaValProSerAsnGlyVal 1678
Db 241 GAAAGAAATAGCGGTGGGCTGAGGAGCTGTGTCGGAAACCTGCTGTCGCCAGTAAGCGGGGTG 300
Qy 1679 LysThrGlyGluArgTyrLeuValAspAspValValSerPheGlnCysGluProGlyTyr 1698
Db 301 AAGCTGGCGAGCGCTGCTGTAATGATGTGTCTTTCAGTGTGACCCGGAGAT 360
Qy 1699 AlaLeuGlnGlyValAlaHisIleSerCysMetProGlyThrValArgArgTyrAsnTyr 1718
Db 361 GCCCTCCAGGGCCAGGCCCATCTCTCGCATGCCGGAACAGTGGCGCGATGGAATCAC 420
Qy 1719 ProProProLeuCysValIleAlaGlnCysGlyGlyThrValGluGluMetGluGlyValIle 1738
Db 421 CCTCTCCACTGTGATATGACAGTGTGGGAAACAGTGGAGAGATGAGGGGGTGCATC 480
Qy 1739 LeuSerProGlyPheProGlyAsnTyrProSerAsnMetAspCysSerTrpValIleAla 1758
Db 481 CTGAGCCCCGGGCTTCCAGGCACTACCCAGTAACATGAGCTGCTCTGAAATAAGCA 540
Qy 1759 LeuProValGlyPheGlyAlaHisIleGlnPheLeuAsnPheSerThrGluProAsnHis 1778
Db 541 CTGCCCGTGGGCTTGGAGCTCACATCCAGTCTTCTGAACCTTCCACCGAACCCACAC 600
Qy 1779 AspTyrIleGluIleArgAsnGlyProTyrGluThrSerArgMetMetGlyArgPheSer 1798
Db 601 GACTACATAGAAATCCGGATGGCCCTCATGAGACACAGCCCATGATGGAAATTCAGT 660
Qy 1799 GlySerGluLeuProSerSerLeuLeuSerThrSerHisGluThrThrValTyrPheHis 1818
Db 661 GGAAGCAGAGCTTCAAGCTCTCTCTCTCCAGTCCAGACACACCGTATTTTCCAC 720
Qy 1819 SerAspHisSerGlnAsnArgProGlyPheLeuGluGluTyrGlnAlaTyrGluLeuGln 1838
Db 721 AGCAGACCACTCCAGAAATCGGCGCAGGATTCAGCTGAGATTCAGGCTTAAGACTTCA 780
Qy 1839 GluCysProAspProGluProPheAlaAsnGlyIleValArgGlyAlaGlyTyrAsnVal 1858
Db 781 GAGTGGCCAGACCCAGAGCCTTTGCCAATGGCATTTGAGAGGAGCTGGCTACACAGTG 840
Qy 1859 GlyGlnSerValThrPheGluCysLeuProGlyTyrGlnLeuThrGlnHisProValLeu 1878
Db 841 GGACAATCAGAGCTTCTGAGTGTCTCCGGGAGTATCAATTGACTGGCCACCTGTCTCTC 900
Qy 1879 ThrCysGlnHisGlyThrAsnArgAsnTrpAspHisProLeuProLysCysGluValPro 1898
Db 901 ACGTGTCAACATGGGACCAACCCGAACTGGGACCACTGCGCAAGTGAAGTCCCT 960
Qy 1899 CysGlyGlyAsnIleThrSerSerAsnGlyThrValTyrSerProGlyPheProSerPro 1918
Db 961 TGTGGCGGAAATCATCACTTCTTCCACGGCACTGTGTCTCCGGGGTTCCTAGCCCG 1020
Qy 1919 TyrSerSerSerGlnAspCysValAlaTrpLeuIleThrValProIleGlyHisGlyValArg 1938
Db 1021 TACTCCAGCTTCCAGGACTGTGTGTGTGATACCCGTCATGGCCATTTGGCCAGGCTCGC 1080
Qy 1939 LeuAsnLeuSerLeuLeuGlnThrGluProSerGlyAspPheIleThrIleTrpAspGly 1958
Db 1081 CTCAACTCAGCTCGCTGCAACAGAGCCCTCTGGAATTTCAATCCATCTGGGAGTGG 1140
Qy 1959 ProGlnGlnThrAlaProArgLeuGlyValPheThrArgSerMetAlaValysThrVal 1978
Db 1141 CCACAGCAACACAGACCAACGCGCTCGGCGTCTTCAACCCGAGACATGGCCAAAGAAACAGTG 1200
Qy 1979 GlnSerSerSerAsnGlnValLeuLeuLysPheHisArgAspAlaAlaThrGlyGlyIle 1998
Db 1201 CAGGATTCATCAACACAGGCTCTGTCAAGTTCCACCGTGTATGACGACACGGGGGATTC 1260
Qy 1999 PheAlaIleAlaPheSer-----AlaTyrPro----- 2007

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Db 1261 TTGSCATAGCTTTCTCCGCTCAGTATGAAAGCTGCTGTGGGAAAGGCCAGGCTTT 1320
Qy 2008 -----LeuThrIysCysProProProThrIleLeuProAsn----- 2019
Db 1321 CAAGTCAAGGCTGAGTGTGACTCCGCTGCACACTTTGGGAGCAATGACCTTGAAGTG 1380
Qy 2020 -----AlaGluValValThrGluAsnGluGluPheAsnIleGlyAs 2033
Db 1381 AGTTGTATTAACCTTTGAGAGCTTCACTGTCTTCAAGATTATGAAATTAAATGATTAGC 1440
Qy 2033 pIleValArg-----TyrArgCysLe 2040
Db 1441 CTATGTAGAGCTCTCAGTGCAGGGTTCTGTAAATGCAAGTTTCTCTATTCACACT 1500
Qy 2040 uProGlyPheThrLeuValGlyAsnGluIleLeuThrCysLeuLeuGlyThrTyrLeuG 2060
Db 1501 GCCAGGG-----CAGAGGGCAGACAGAACCCA 1527
Qy 2060 nPheGluGlyProProProIleCysGluValHis----- 2071
Db 1528 AACCTTGTGCTCAAGTCCACTCATTCATCAATCACTCACTGCTGGATCATCTTACT 1587
Qy 2072 -CysProThrAsnGluLeuLeuThr 2079
Db 1588 GTGCCCAAGCTTATCCCTTAGCACT 1612

RESULT 15
US-09-911-842-3
; Sequence 3, Application US/09911842
; Patent No. US20020151483A1
; GENERAL INFORMATION:
; APPLICANT: Welcher, Andrew A.
; APPLICANT: Eliott, Gary S.
; TITLE OF INVENTION: C3B/C4B COMPLEMENT RECEPTOR-LIKE MOLECULES AND USES THEREOF
; FILE REFERENCE: 01017/37592
; CURRENT APPLICATION NUMBER: US/09/911,842
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: US 60/222,438
; PRIOR FILING DATE: 2000-08-01
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 11230
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-911-842-3

Alignment Scores:
Pred. No.: 2,29e-159 Length: 11230
Score: 1852.00 Matches: 808
Percent Similarity: 31.44% Conservative: 374
Best Local Similarity: 21.49% Mismatches: 1215
Query Match: 10.90% Indels: 1363
Gaps: 9

US-10-016-248-2 (1-3104) x US-09-911-842-3 (1-11230)
Qy 74 CysProAspProGlyIleProGluArgGlyLysArgLeuGlySerAspPheArg----- 91
Db 1310 TGTCTTCCGCTCGAAGCTCTCGAAGAAATGTTTTTTATACAAACACTTGCAGAAACCTAC 1369
Qy 92 LeuGlySerSerValGlnPheThrCysAsnGluGlyTyrAspLeuGlnGlySerLysArg 111
Db 1370 TTCATATCCCGCTGTGGGCTCGATGTGCGCCGGGCTTTGACCTTGGGAGAGCAGATC 1429
Qy 112 IleThrCysMetLysValSerAspMetPheAlaAlaTrpSerAspHisArgProValCys 131
Db 1430 CATTGTGTCAACCC-----AATGCTTTGTGTGCTGGGACAGAAAGCTTCTGC 1477
Qy 132 ArgAlaArgMetCysAspAlaHisLeuArgGlyProSer---GlyIleIleThrSerPro 150
Db 1478 AGAGTGAAGACGTGC-----CCCACTCTCGAACAGCCAAACAGGCGCACATCAGCTGTCC 1534

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QY 151 AsnProGluGlnIleuValAspAsnAlaHisCysValTrpIleIleThrAlaLeuAsn 170
 Db 1535 ACTGCGAAATGCTCTAC-----AACACCTGTGT-----TTGGTTACCTGC----- 1576
 QY 171 ProSerIleValIleuValaPheGluGlnPheAspLeuGluArgIleuValAspThr 190
 Db 1577 -----AATGAAGATACAGATT 1594
 QY 191 LeuThrValGlyAspGlyGlyGlnAspGlyAspGlnIleuValLeuIleuValMetSerGln 210
 Db 1595 -----GAAGCAGACCTAGCTTACCTGTCAGAGA 1624
 QY 211 AsnAlaCysSerAspSerProHisThrProGlySerArgIleProGluSerMetSerGly 230
 Db 1625 AATGCCAGTGGAGTGGCCCGAGAG-----CCCGGCTGTGAAG-- 1663
 QY 231 AspIleTrpArgGlnIleuValTrpThrValLeuGlnIleCysArgAspIleSerSerSerAsp 250
 Db 1663 ----- 1663
 QY 251 AlaArgSerGlySerValaArgIleuValSerProIleuValSerAsnAlaValGluLeuValAla 270
 Db 1664 ---CGCATTTGTGCGACCTTCCAGAACCCCAA----- 1693
 QY 271 ProGlyThrGluIleGluGlnIleuValSerCysGly---AspProGlyIleProAlaTrpGly 289
 Db 1694 ---GGCTCATCTTTTCTCCACCCAGCTGCGCAGAGAGCCCGCAGGCTT----- 1741
 QY 290 ArgArgGluGlySerArgPheHisGlyAspThrLeuValPheGluCysGlnProAla 309
 Db 1742 -----GGGATGACCTGTGACCTTAAGCTCCCGCAGGGA 1774
 QY 310 PheGluLeuValGlyGlnIleuValaIleThrCysGlnIleuValAsnGlnIleuValAspThr 329
 Db 1775 TACATTTTATCCGGGAGTCAAGAAAGTGAAGTGCACATCTGGAGAGTGAAGTGCAGAA 1834
 QY 330 ---LysProGlyCysValPheSerCysPhe----- 338
 Db 1835 GTTCAGACAGCTGTGTCAAAAGTGTGGAGCTCCCAATCAGCTGTCCAAATGACATT 1894
 QY 339 -----PheAsnPheThrSerProSer--- 345
 Db 1895 GAGGCAAAAGATGGGAGCAGCAGAGACTGTCTAATGCTCAGCAGTGCACCAAGCTCAAGCT 1954
 QY 346 -----GlyValValLeuSerProAsnIleuValAspThr--- 357
 Db 1955 AAAGCAACTCTGTGTAAGAGTGTCT---AGTCACTGCCACCCAGCTTTTACCCCA 2008
 QY 358 -----GlyAsnHisLeuHisCysValaTrpLeuIleLeu 369
 Db 2009 CTTTACCTTCCCAATTGAGAGACGTGGCCATCACCCTACACGGCAACCCAGCTATC----- 2064
 QY 369 LysArgProGluSerArgIleHisLeuAla-PheAsnAspIleAspValGluPro----- 386
 Db 2065 ---CGGTAACCAACCCAGCTGCACTTTCTACATTAGGTCAATGATGTGAACCGCTGTCT 2122
 QY 387 -----Gln 387
 Db 2123 ATAGATTGGTGGCGATCTCCACTCCAAATCCAGGTGTGAGAGAGACCCCTGCAGAC 2182
 QY 388 PheAspPheLeuValIleuValAspGlyAlaThrAlaGluAlaProValLeuGlyThrPhe 407
 Db 2183 TGGATGAGGCTCAGTTCTCAGACAACTCGGGGCTGAATGTGCTATTACAGAGACTCAG 2242
 QY 408 Ser---GlyAsnGlnLeuProSerSerIleThrSerSerGlyHisValaAlaArgLeuGln 426
 Db 2243 ACACAAGGCGACATGTTTCTCATGGGAAACGGTGTGTGTGTAACACAGCC----- 2293
 QY 427 PheGlnThrAspHisSerThrGlyLysArgGlyPheAsnIleThrPheThrPheArg 446
 Db 2294 -----ACTGACCCCTCAGGCAACAAGAGACTGTGACATC---CACATTGTCATATAA 2344

QY 447 HisAsnGluCysProAspProGlyValProValAsnGlyLysArgPheGlyAspSerLeu 466
 Db 2345 GGTTCCTCCGTGAGGTCCCTTACCCCTGTAAAGGGAGACTTTATCTGTGCCAGAT 2404
 QY 467 GlnLeuGlySerSerIleSerPheLeuValAspGlyGlyPheLeuGlyThrGlnIleuVal 486
 Db 2405 AGTGTGAGATTAACTGTAGCCCTGAGCTCAGAGAGGCTTATGATTTCACAGAGGTCA 2464
 QY 487 ---GluThrIleThrCysValLeuValGlyGly-----SerValVal 499
 Db 2465 CCTGAGAAAGTACTACTGTCTTTGAAAGATGTGATCTGAGACACACCATATCTACAGA 2524
 QY 500 TrpAsnSerAlaValLeuArgCysGlyAlaProCysGly----- 512
 Db 2525 TGGCCAGACTGTGCTATAAAGGTTTGTCAAAACATGGTTTCAAGTCTTTGAATGCTA 2584
 QY 513 -----GlyHisLeuThrSerProSerGly 520
 Db 2585 TACAAACACATCGCTGTGATGACATGATCTGTTAAGAGTTTCTGCAGATTGAG 2644
 QY 521 ThrIleLeuSerProGlyTrpProGlyPheTrpLysAspAla----- 534
 Db 2645 ACTACCTGTGGGAAACATGTGCTCCCTTTGTAAAGATGTGATGACATGACATGACAGA 2704
 QY 535 -----LeuSerCysAlaTrpValIleGluAlaGlnProGlyTrpPro----- 548
 Db 2705 CTGAGAGACTTACCAAAATATCTGATCGAGTATTAATTACACATGATAAATGGCTTT 2764
 QY 549 -----IleValIleThrPheAspArgPhe 556
 Db 2765 GCAATTGACACAGAGGTGGGTGACAGCAACAGAGCTGAGATTATCTGACATGACTTC 2824
 QY 557 LysThrGluValAsnTrpAspThrLeuGluValaArgAspGlyArg----- 571
 Db 2825 CTGGATGTTGTACAGAAACACCCACGATGTGGCAAGCCAGATCTGCACAGATTAA 2884
 QY 572 -----ThyTrpSerAla 575
 Db 2885 AGAAGTGTCCATGTGTGACCCCAAAATTCAGTAAATTTTAAATCAGCTAGCTGAGCTG 2944
 QY 576 ProLeuIleGlyValaTrpHisGlyThr-----GlnValProGlnPheLeuIleSer 592
 Db 2945 CCATCTCCAGAGAAAGAAACGATACCTTGAATGTGAAGATCAGACAGGACTCATTAAG 3004
 QY 593 Thr-----SerAsnTrpLeuTrpLeuPheSerThrAspIleSerHisSer 608
 Db 3005 ACATTGAAACATGACCAATGCTGTAAGAACGACTTGAATTAAGAGCCCATGTATTCT 3064
 QY 609 AspIleGlyPheGlnLeuArgTrpGluThrIleThrLeuGlnSerAspHisCys----- 626
 Db 3065 ---TTCCAGCTGCTCGGAAACAGTGTGGCTGACAGCAATTCCTCGAAACA 3115
 QY 627 -----LeuAspProGlyIleProValAsnGlyGlnArg----- 637
 Db 3116 GAAAGGCTTTCTCTTCTGACAGACAGGCTCTGTGAGGGGGCGATGTGTCAAC 3175
 QY 638 -----HisGlyAsnAspPheTrpValGlyAlaLeuValIleThrPheSerCysAspSerGly 655
 Db 3176 TGCCCCCTGGGAAACCTTTACTCTCTTGAGAGATTCCACTGTGAAGAGCTGCTCATGGGA 3235
 QY 656 TyrThrLeuSerAspGlyGluProLeuGluCysGlu-----Pro 668
 Db 3236 TCTTACCAAGATGAAGAGGAGAGCTGGAATGCAAGCTCTGTCCCCCAAGACTACAGCG 3295
 QY 669 AsnPheGlnTrpSerArgAlaLeuProSerCysGluAlaLeuCysGlyGlyPheIleGln 688
 Db 3296 GAATACCTCCCATTCAGAAAGGCTCTGAATGCAAAAGCTCAGTGAAGCAAGACACTAC 3355
 QY 689 GlySerSerGly----- 692
 Db 3356 TCTTCAAGTGGCTGAGAGACTGGAATGCTGTCCGCTGGTACTTATCAACCGGAATTT 3415
 QY 693 -----ThrIle----- 694

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Db      3416 GGATCCGGAGCTGCTCTCTATGCCAGAAACACACACGCTGAAAAGAGCCGTG 3475
Qy      695 -----Leuser 696
Db      3476 GACATCTCTGCTTGAGAGTCCCTGCCAGTAGAGAAATTCCTCCGTTCTGGCTAACA 3535
Qy      697 ProlylPhePro-----AspPheTyrProAsnAsn-----Leu 707
Db      3536 CCCGCTACCTCTGCTCCCTCGAGACTATTACCAACCCATGACAGGAACTCTTCTGCTC 3595
Qy      708 AsnCyThrTyr-----711
Db      3596 GCTTGCTCCTTTATGAACTACAAACATCACTGGCCGAGCTCATTCACAGACTGTCA 3655
Qy      712 -----IleIleGluThrSer 716
Db      3656 AGTTTAGCTCTACTTTCTCAGACAGAAAGAAAGATAGTCCCTGCTGCGCCCTGGA 3715
Qy      717 HisGlyysGlyValPhe-----PheThrPheHisThrPheHisLeu-----730
Db      3716 CATTCACGAACAAGTACGAAGTACGACGAGCTTTTACGAATGCTTTTAAACCCC 3775
Qy      731 -----GluSerGlyHisAspTyrLeuLeuIleThrGluAsn 742
Db      3776 TGCACAAACAGTGAACCTGCCAACAGCTTGGCGGTGTTATGTCTGTCTGCCACCT 3835
Qy      743 GlySerPheThrGlnProLeuArgGlnLeuThrGly-----754
Db      3836 GGA-----TACACAGCTTAAAGTGTGAACAGATATTGAT 3871
Qy      755 -----SerArgLeuProAlaProIleSerAlaGlyLeu-----TyrGlyAsn 768
Db      3872 GAATGACGCTCTGCTTGC-----CTCATGTGTGAATTGTAGAACCAAGTTGGGGA 3928
Qy      769 PheThrAlaGlnValArgPhe-----775
Db      3929 TTACACGCGCAATGTTCAATTGGGCTATTACAGTCAAAATATGTGAAGAAATATTAATGAC 3988
Qy      776 -----IleSerAspPheSerMetSerTyr-----783
Db      3989 TGTATCTCAGACCTTGCTTAATAAAGAACTGACGCTGACGGCTTGGACGTAACGCC 4048
Qy      784 -----GluGlyPheAsnIleThrPheSerGlyTyrAspLeuGlnProCysGlu 799
Db      4049 TGTACTGTGTGAAGATACATGAGTGTGCACTGTGAACAGCTGAATGAATGCCAG 4108
Qy      800 GluProGluValProAlaTyrSerIleArgGlyLeuGlnPheGlyValIleGlyAspThr 819
Db      4109 TCAAGCCCCCTGCTTAACACAGCAGTTGTAAAGCAAGTTGGGGG-----4156
Qy      820 LeuThrPheSerCys-----PheProGlyTyrArgLeuGlnGlyThrAla 834
Db      4157 -----TTCTGCTCAAAATGCCCAACCGGATTTTGGGTACTCGGTGTGAAAAAATGTG 4210
Qy      835 -----ArgIleThrCysLeuGlyValArgArgArg 844
Db      4211 GATGAGTGTCTCACTACGACCATGCCAAATGAGACCACTTGTAGAGATGGCCAAACAGC 4270
Qy      845 LeuTrpSerSerProLeuProArgCysValAlaGluValAsnSerValIleThrGlyThr 864
Db      4271 TTC-----AGGTGT-----CAATGTCCAGCAGGCTTACACGGGACA 4306
Qy      865 GlnGlyThrLeuLeuSerProAsnPheProValAsnTyrAsn-----878
Db      4307 CACTGTGAACGT-----AACATCAACGAGTGCAGTCCAAACCGC 4345
Qy      879 -----AsnAsnHisGlyCysIle-----TyrSerIleGlnThrGlnPro 891
Db      4346 TGTAGAAACAGGCGCACCTGTGTGATGAATACTCATACAGTGTGAATGTGCAGCA 4405
Qy      892 GlyysGlyIleGlnLeuValAlaArgAlaPheGluLeuSerGlnGlyAspValLeuLys 911

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Db      4406 GGA-----TTTTCAGGCCACAGGTGTGAGACAGAACAGCT-----4441
Qy      912 ValTyrAspGlyAsnAsnAsnSerAlaArgLeuLeuGlyValPheSerHisSerGluMet 931
Db      4442 -----TCCGATTTTAACTGTGATTTGAAGTTTCTGGCATCTACGGGTAGCTCTGCTA 4495
Qy      932 MetGlyVal-----ThrIleAsnSerThrSerSerLeuThrPleu-----Asp 946
Db      4496 GATGAGTGTCTGCCAACCTCTCATGCGGTACCTGCGCATTTCTGATGAATCTCTGAT 4555
Qy      947 PheIleThr-----AspAlaGluAsnThr-----954
Db      4556 GTCATCAACTACGGGAGCCCATCTCCATGCACTTGAAGATGACAAAGAACACACCTTC 4615
Qy      955 -----SerIysGlyPheGlnLeuHisPheSerPheGluLeuIle-----968
Db      4616 CTCTGACTGATTTCAACAGCGGTGGTTCTTATGTGAATGGAAGAAAGATCACCAC 4675
Qy      968 -----968
Db      4676 TGCCCTCCGTAATGATGCGCATTTGGCATCATTTGCAATCAGATGACAGATTTGGT 4735
Qy      969 -----LysCysGluAspProGlyThr-----975
Db      4736 GAGCCTGAGAGGCTATATATGATGGGAATTATCTACGCTGCTTCCATTT 4795
Qy      975 -----975
Db      4796 GGCAAAGCCATACCTGTGGCGGTGATTAATTCTTGGCAAGACAAACAAAAGGA 4855
Qy      975 -----975
Db      4856 GAGGGTTCAACCCGCTGAGTCTTTTGTGGCTTCATTAAGCAGCTCAACTCTGGGAC 4915
Qy      975 -----975
Db      4916 TATGCTGTCTCAGACAGGTGAAGTTGTGGCCAGCTCTGCCAGAGAACTGAGT 4975
Qy      976 -----ProlyAspPhe-----GlyTyrLysVal 982
Db      4976 CGGGAAACGTGTAGACATGCGCCGATTTCTGTGGGAATCACGGGGAAGTGAAGGTT 5035
Qy      983 HisAspGlnGlyHisPheAla-----989
Db      5036 GATTCCAGACGATGTTCTGCTGATTTGCTCGTCTTTAGAGATCCGTCCTCACCTG 5095
Qy      990 -----GlySerSerValSerPheSerCysAspProGly 1000
Db      5096 AGACCTGCATCAGGAATTCGAAAGCCAGGCTCCAAAGTCACTGCTGTGATCCGGGC 5155
Qy      1001 TyrSerLeuArgGlySerGlnLeuLeuCysLeuSerGlyValArgArgThrTyrAsp 1020
Db      5156 TTCCAGATGTTGGGATCTCTGTCAGTATGTCTGAAC-----CAAGGCACTGACACA 5209
Qy      1021 ArgProLeuProThrCysVal-----AlaGlnCysGly-----GlyThrValArgGly 1036
Db      5210 CAACCACTCCCCCACTGTAACCGATTCGCTGTGGGCTGCTCCGCTTGGAGAAATGGC 5269
Qy      1037 GluValSerGlyGlnValLeuSerProGlyTyrProAlaProTyrGlnHisAsnLeuAsn 1056
Db      5270 TTCTACTCAGCGGAGACTTCATCGCGGACGACGAGTACTGAG-----5317
Qy      1057 CysIleThrThrIleGlnAlaGlnAlaGlyCysThrIleGlyLeuHisPheLeuValPhe 1076
Db      5318 -----TGCAACAGTGGC-----TACTACTCTGCTGGT 5344
Qy      1077 AspThrGlnGlnValHisAspValLeuArgIleThrAspGlyProValGluSerGlyVal 1096
Db      5345 GATTCCGAATGTTTCTGCRACAGACACGAGAGCTGAACGCAATTTCACCATCTGTCTC 5404
Qy      1097 LeuLeuLysGluLeuSer-----1102
Db      5405 GATGTCATATAGTGTGACATGCGCTCGGACTGTATGAGACACGCTCTGCTGAACACC 5464

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QY 1102 ----- 1102
Db 5465 AACGATCTACGATGCTCTGTGAACCCACCATACAGGAGATGGAAAACTGTGCA 5524
QY 1103 ----- GlyProAlaLeuProIysAspLeuH1SerThrPheAsnSer 1116
Db 5525 GAACTGTAAATGATTAAGGCTCCAGAAAAATCCAGAAAAATGGCCGCTCT 5572
QY 1117 ValValLeuGlnPheSerThrAspPheSerThrSerIysGlnGlyPheAla1IleGlnPhe 1136
Db 5573 ----- TCTGGCGAGATTACACC-----GTGGGTACTGCAGTCCACATT 5611
QY 1137 Ser-----ValSerThrAlaThr----- 1142
Db 5612 TCCGTGTACGAAGGGACAGACGTGTGGAGATGACACATCACTGTGTTGGACACTGCC 5671
QY 1143 -----SerCyAsnAspProGlyIlePro 1150
Db 5672 GAGTGGATCCGCTCAGCCGCTCTGTGAAGCCATTCTCTGTGGTGTCCACCTGTTCT 5731
QY 1151 GlnAsnGlySerArgSerGlyAspSerTrpGlnAlaGlyAspSerThrValPheGlnCys 1170
Db 5732 GAAATAGTGTTGTTGACGGGTCCGCAATCAATATGACATAGAGTGGTGTACAGGTGT 5791
QY 1171 AspProGlyTyrAlaLeuGlnGlySerAlaGlnIleSerCyAsnValIys1IleGlnAsnArg 1190
Db 5792 GATTAAGGATATCTTGTGTGGGATGAAGATCAGCATGCTGTCTAGTGGTTC-- 5848
QY 1191 PheSerTrpGlnProSerProProThrCys--1LeuAlaProCysGlyIleAspLeuThr 1209
Db 5849 -----TGGAGTCAATTCCTCTCTGTGGTGGCTAGTGAAGTGT----- 5887
QY 1210 GlyProSerGlyValIleLeuSerProAsnTyrProGlnProIleProGlyIysGln 1229
Db 5888 -----TCCAGCCTTAGACATTAATAACGGCAAA-- 5917
QY 1230 CysAspTrpIlyValThrValSerProAspTyrValIleAla-----LeuAla 1245
Db 5918 -----TACATCTTAAGTGGGCTCACCTACCTTTCT 5947
QY 1246 PheAsnIlePheAsnLeuGlnProGlyTyrAspPheLeuH1IleTyrAspGlyArgAsp 1265
Db 5948 ATTGCACTGATCTCTGTGAGAACGATACAGTTTA----- 5983
QY 1266 SerLeuSerProLeuIleGlySerPheTyrGlySerGlnLeuProGlyArgIleGlySer 1285
Db 5984 -----CAGGGCCCATCCCTCTTGAATGC 6007
QY 1286 SerSerAsnSerLeuPheLeuAlaPheArgSerAspAlaSerValSerAsnAlaGlyPhe 1305
Db 6008 ACAGCTTCCGCGCAGCTGG-----GACAGAGCGCCACCTAGCTGCAACT 6052
QY 1306 ValIleAspTrpThrGlnAsnProArgGlnSerCysPheAspProGlySerIleIysAsn 1325
Db 6053 GTC-----TCTGTGGAGAGCGCTCCAAATGCAAAAGAT 6085
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Db 6086 GCTGTCACTACCTGGAGCAACTTCACTTTGGAGACAGTTCCTTACATGCAAAAG 6145
QY 1346 GlyTyrGlnValGlnGlyThrSerThrLeuSerCysIleLeuGlyProAspGlyIysPro 1365
Db 6146 GGGTACACCTTGTCTGGGCTTACACCATCATATGC-----CAGGCAACGGCAAA-- 6196
QY 1366 ValTrpAsnAsnProArgProValCysThrAlaProCysGlyIleGlnIlyrValGlySer 1385
Db 6197 -----TGAATTCAGTAAACCAACCACTGCTGCT 6226
QY 1386 AspGlyValValLeuSerProAsnTyrProGlnAsn-----TyrThrSerGlyGlnIle 1403
Db 6227 -----GTCTCTGTGTACGAGCCCGCCCAATGTGAGACACAGCCCTCTCCAGAGACT 6274

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QY 1424 HisThrAlaLeuAsnAspValValGluValH1AspGlyH1SerGlnHisSerArgLeu 1443
Db 6308 TACTGTGCG-----GATGGCTTACAGC----- 6328
QY 1444 LeuSerSerLeuSerGlySerHisThrGlyGlnSerLeuProLeuAlaThrSerAsnGln 1463
Db 6329 -----CTGGCTGATATATCCAG 6346
QY 1464 ValLeuIleIysPheSerAlaIysGlyLeuAlaProAlaArgGlyPheHisPheValTyr 1483
Db 6347 CTCATGTCAATGCCAGGAGAACTGGGTCCCGCGCGGC----- 6388
QY 1484 GlnAlaValProArgThrSerAlaThrGlnCysSerSerValProGlnProArgTyrGly 1503
Db 6389 CAGGCTGTCCGCGCTGATAGTCACTTCTGTGAAAACCCCAATCTGTTCTCTACAG 6448
QY 1504 -----LysArgLeuGlySerAspPheSerValGlyAlaIleValArgPheGlnCys 1520
Db 6449 ATCTTGAATCTGTAGCAAAAGCAAGTTTGCACCTGCTCGTATGTAGCTTCAAGTGC 6508
QY 1521 AsnSerGlyTyrAlaLeuGlnGlySerProGlnIleGlnCysLeuProValProGlyAla 1540
Db 6509 ATCGAGGTTTGTCTGTGAACCTCAGGAAGATTGAATGCTTGA----- 6556
QY 1541 LeuAlaGlnTrpAsnValSerAlaProThrCysValAlaProCysGlyIleAsnLeuThr 1560
Db 6557 -----GGTGAAGATGGAGC 6571
QY 1561 GluArgArgGlyThrIleLeuSerProGlyPheProGlnProTyrLeuAsnSerLeuAsn 1580
Db 6572 -----CTTCTCCCTC-----TGGGTCCAG 6592
QY 1581 CysValTrpIlyIleValValProGlnGlyAlaGlyIleGlnIleGlnValValSerPhe 1600
Db 6593 TGC----- 6595
QY 1601 ValThrGlnGlnAsnTrpAspSerLeuGlnValPheAspGlyAlaAspAsnThrValThr 1620
Db 6595 ----- 6595
QY 1621 MetLeuGlySerPheSerGlyThrThrValProAlaLeuLeuAsnSerThrSerAsnGln 1640
Db 6596 -----ATCCGAGTG----- 6604
QY 1641 LeuTyrLeuHisPheTyrSerAspIleSerValSerAlaAlaGlyPheHisIleuGlnTyr 1660
Db 6604 ----- 6604
QY 1661 LysThrValGlyLeuSerSerCysProGlnProAlaValAlaProSerAsnGlyValIlyThr 1680
Db 6605 -----CGATGCGAGAGGCTCCACATCGCAATGGCTACCCGAGT 6646
QY 1681 GlyIleArgTyrLeuValAsnAspValValSerPheGlnCysGlnProGlyTyrAlaLeu 1700
Db 6647 GGGAAACATACAGTTTGGGCGCGTGTGGCTTACAGTCCACAGAGATTTCTATATC 6706
QY 1701 GlnGlyHisAlaHisIleSerCysMetProGlyThrValaArgArgTrpAsnTyrProPro 1720
Db 6707 AAGGGGAGAGAGAGACAGCTGT-----GAGGCAACAGACAGTGGAGAAACCCAG 6760
QY 1721 ProLeuCysIleAlaGlnCysGlyIleThrValaGlnGlnMetGlnGlyValIleLeuSer 1740
Db 6761 CCCACTGC----- 6769
QY 1741 ProGlyPheProGlyAsnTyrProSerAsnMetAspCysSerTrpIlyIleAlaLeuPro 1760
Db 6770 -----CATCT-----GTGCTCTGTAAACGAGCCACTTAAGTTGAG 6805
QY 1761 ValGlyPheGlyAlaHisIleGlnPheLeuAsnPheSerThrGlnProAsnHisAspTyr 1780

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Db	6806	AACGGCTTCC	TGGAGCACCA	CTGGCAGAC	CTTTGAGAC	GGAAGCTT	CCAGTGC	6865
Oy	1781							
Db	6866	-----	---ACCCAGGCTTA	AGCA-----			---GCCGAGAT	6892
Oy	1801							
Db	6893	-----	---CCTGATGTTGTTG	CCAGCAACCA	TGC-----	CACTGGCAGAC	GGCAC	6934
Oy	1821							
Db	6935							
Oy	1841							
Db	6965							
Oy	1861							
Db	7025							
Oy	1881							
Db	7085							
Oy	1899							
Db	7136							
Oy	1918							
Db	7184							
Oy	1938							
Db	7238							
Oy	1958							
Db	7283							
Oy	1978							
Db	7285							
Oy	1998							
Db	7286							
Oy	2015							
Db	7325							
Oy	2035							
Db	7382							
Oy	2055							
Db	7442							
Oy	2074							
Db	7496							

Db	7589	-----GTGGCAATGCTACACCTCTGTGGG	7615
Qy	2134	ProSerGIgYln-----SerProLeuLeuYsAlaLeuSerGIYAsnTyrSer	2149
Db	7616	GAATAATGCCAGTGGCTCGAGAAACCAATGTGCAAAACCAATTGAA-----	7663
Qy	2150	AlaProLeuIleValThrSerSerSerAsnSerValTyrLeuAlgtTpsSerSerAspHis	2165
Db	7663	-----7663	
Qy	2170	AlaTyrAsnArgIysGIYPhenylIleArgTyrSerAlaProTyrCySerLeuProArg	2189
Db	7664	-----TGCCAGAGCCCAAG	7678
Qy	2190	AlaProLeuHISGIYPhenIleLeuGIYlnThrSerThrGlnProGIYGIYSerIleHis	2209
Db	7679	GAGATTTAAATGGC---CAATTCTCTCCGTGAGCTTTGAGTATGGCAAAACCATGCA	7735
Qy	2210	PhenGIYCyAsnAlaGIYTYrArgLeuValGIYHisSerMetAlaIleCySerThrArgHis	2229
Db	7736	TACTTTTGTGACCGGGGCTTCGGCTCGAAGGTCCAAATCCCTGACCTGTTTAGAGACA	7795
Qy	2230	ProGlnGIYTYrHisLeuTpsSerGluAlaIleProLeuCyGlnAlaLeuSerCyGIY	2249
Db	7796	GGTGCAC-----TGGAGATATGGATCCCCCTCTTGTATGTCACATCAGCT	7843
Qy	2250	LeuProGluAlaProLYAsnGIYMetValPhenGIYSGIYTYrThrValGIYThrLYs	2265
Db	7844	GACCACAGCCCATTTGAAATGTGTTTCTTAAGAGTGGGATTCAGATAGGTCGCATG	7903
Qy	2270	AlaValTYrSerCySerGIYGIYTYrHisIleGlnAlaGIYAlaGIYAlaThrAlaGIY	2289
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Qy	2290	CysLeuAspThrGIYLeuTpsSerAsnArgAsnValProProGlnCyValProValThr	2309
Db	7958	TGTGAAGAGTGGGA--TGTCAAGCTCCAGC-----CCAACCTGTGATCCCATAGAC	8008
Qy	2310	Cys-----ProAspVal-----SerSerIleSerValGlnHISGIYArgTps	2323
Db	8009	TGCGGTCTCCCTCTCCACATAGACTTTGGTACGTACTAAGTCAGAGATGGCCAGGA	8068
Qy	2334	ArgLeuIlePhenIle-----2328	
Db	8069	CATTGTGATCAAGAAATGATGATGAGAAATCCATATCTGGCTACCTCAACATTTG	8128
Qy	2339	-----ThrGln	2330
Db	8129	GAAGCAACAGTAAAGCCTTGAAAAATCAAAAGAGTCGCTGCCTCACATGATCCAC	8188
Qy	2331	TyrGlnPhenGlnAlaGlnLeuMetLeuIleCyAspProGIYTYrTYrTYrThrGIYGIYln	2356
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Qy	2351	ArgValIleArgCySGlnAlaAsnGIYLYsTpsSerLeuGIYAspSerThrProThrCys	2370
Db	8249	CGTGCGTCAATCTGCGCAAGAGATGTCGTGGAAT-----GGTACCGCACCTCTTGG	8302
Qy	2371	ArgIleIleSerCySGIYGIYLeuProIle---ProProAsnGIYHisArgIleGIYThr	2389
Db	8303	ATTTCCATTGATGATG--GATTTCTGTGTTCTCCCGAAATGTGCTTTTTCATTTTCA	8359
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Db	8360	CAGACGACTATGGGCAAGTCTGCGACAAATATAGCTGCAAGCCGGGACACATTTTGAAAGC	8419
Qy	2410	SerArgValArgGIYCyMetAlaAsnGIYLeuTpsSerGIYSerGIYValArgCysLeu	2429
Db	8420	TCCCACTTAAGACTCTGTCTCGACAGATTAAGCAGTGGAGTGCACGTGTCACGCTGTGAA	8479
Qy	2430	AlaGIYHisCySGIYTYrProGlnProIleValGlnGIYHisIleAsnGIYLeuAsnTYr	2449
Db	8480	GCCATCTCATGACAGTAACCAACCCACTCTGAGATGGATTCATCAACAAAGGATGACATTC	8539

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 DB 8540 TCCTACCTGGGTGGTGTATTAAGAGTGTGACCTGGCTATATTCATAGGCTCTTAAG 8599
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 QY 2610 ValSerCysGlyHisProGlySerProProHisSerGlnMetSerGlyAspSerTyrThr 2629
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 QY 2630 ValGlyAlaValAlaArgTyrSerCysIleGlyLeuArgThrLeuValGlyAsnSerThr 2649
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 DB 9125 AGAAGATGCTTCCCATGTGTTCTGTGAGGCACTGCGCATCTGCTTACCTTCAG 9184
 QY 2666 -----SerGlyThrSerValGlyVal----- 2672
 DB 9185 TGTTCCACACCCATCATTTCAACAGGAAACCATCAACGCACTGATTTGGATGTGAAAG 9244
 QY 2672 ----- 2672
 DB 9245 ACGGTCCAGATGTAGTCTTCAAAAGGCTTCAGCTGTGGAATTCGTAATCACCTGT 9304
 QY 2673 -----CysGlyAsp----- 2675
 DB 9305 GATGCCAATGGCCAATGTCTGACGTCCACTGTGTAGACACGCTCAGTGGCGGCTCTC 9364
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 QY 2716 AsnGlySerThrPheSerGlySerGlnProGlyValIleSerGlyAsnProGly 2735
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 QY 2736 ThrProSerAsnAla----- 2740
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QY 2740 ----- 2740
 DB 9602 AGGTGTCTGAAAGGATATGTATGATTTGGATACAGATACATTAACCTGCCAGCAAGAT 9661
 QY 2740 ----- 2740
 DB 9662 GGCATTTGGGTCCCTGAAGATACCTGACAGTCTTAAAAAATGCCCTGTGCATCAAC 9721
 QY 2741 -----ArgValAlaPhe---SerAspGlyLeuValPheSerSerIleValTyrGlu 2757
 DB 9722 ATGACACGATACGTTTTCACGAGATGACTTCCAGTGAACAGCAACATTTCTGTGTCA 9781
 QY 2758 CysArgGlnGlyTyrTyrAlaThrGlyLeuLeuSerArgHisCysSerValAsnGlyThr 2777
 DB 9782 TGTGCAAGAGGTTTATCCACAGAGAGTGAATGTCTCAACATGCCAGCCCAAGTTTCA 9841
 QY 2778 ThrThrGly-----SerAspProGlyCysLeuValIleAsnCysGlyAspProGlyIle 2795
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 QY 2836 ArgThrTyrAsnGlyThrIleProValCysValAlaLeuMetCysValSerProProLeu 2855
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 QY 2856 IleProAsnGlyLeuValValGlySerAspPheMetTyrGlySerSerValThrTyrAla 2875
 DB 10076 TTTCCAAATGGAGAGCTGTCTTGAAGAACACCAATCTGACCAAGCTTGTGTTTTC 10135
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 QY 2915 SerArgGlyArgArgGlnAspArgGlyPheSerTyrArgSerSerValSerPheSerCys 2934
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 QY 3035 ThrHisAlaAsnValGlyAlaLeuAspLeuProSer----- 3046
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 QY 3047 MetGlyTyrThrLeuIleThrProAlaArgArgAlaSerProSerArgValAlaProSer 3066

Tue Oct 19 14:34:57 2004

us-10-016-248-2.rnpb

Page 45

Db 10646 ATGGAGAGCTCTCTT-----GAAAGCCATTATGCATCTCCCTCT 10687
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 18, 2004, 09:55:06 ; Search time 462 Seconds

(without alignments)
4775.517 Million cell updates/sec

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Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1797.5	10.6	10878	4	US-09-911-842A-1
3	1384	8.1	11272	4	US-09-341-461-1
4	1371	8.1	6951	4	US-09-023-655-1265
5	1371	8.1	7313	4	US-09-620-312D-259
6	1362	8.0	6951	6	5256642-1
7	1362	8.0	6951	6	5472939-1
8	1133	6.7	5420	6	5256642-3
9	1133	6.7	5420	6	5472939-3
10	892.5	5.3	3934	4	US-09-023-655-1066
11	779.5	4.6	4661	4	US-09-285-385C-3
12	769.5	4.5	5145	3	US-08-991-408-1

13	769.5	4.5	5145	3	US-09-432-473-1	Sequence 1, Appli
14	768.5	4.5	3919	2	US-08-866-650-4	Sequence 4, Appli
15	768.5	4.5	3919	2	US-09-021-287-4	Sequence 4, Appli
16	768.5	4.5	3919	3	US-09-240-473-4	Sequence 4, Appli
17	764.5	4.5	5021	4	US-09-285-385C-1	Sequence 1, Appli
18	760.5	4.5	3461	4	US-10-140-002-1199	Sequence 19, App
19	740.5	4.4	4771	2	US-08-866-650-2	Sequence 2, Appli
20	740.5	4.4	4771	2	US-09-021-287-2	Sequence 2, Appli
21	740.5	4.4	4771	3	US-09-240-473-2	Sequence 2, Appli
22	725	4.3	3546	3	US-08-872-157-3	Sequence 3, Appli
23	725	4.3	3546	4	US-09-850-048A-3	Sequence 3, Appli
24	712	4.2	3162	4	US-10-140-002-111	Sequence 11, App
25	666.5	3.9	3142	1	US-08-110-158-3	Sequence 3, Appli
26	666.5	3.9	3142	4	US-09-023-655-1090	Sequence 1090, Ap
27	666.5	3.9	3142	5	PCT-US91-05055-1	Sequence 1, Appli
28	663	3.9	3630	3	US-08-991-408-3	Sequence 3, Appli
29	663	3.9	3630	3	US-09-432-473-3	Sequence 3, Appli
30	531	3.1	3834	3	US-09-209-668-18	Sequence 18, Appli
31	531	3.1	3854	1	US-08-365-470-1	Sequence 1, Appli
32	531	3.1	3858	2	US-08-344-155C-98	Sequence 98, Appli
33	531	3.1	3858	3	US-09-009-490A-88	Sequence 88, Appli
34	529	3.1	3863	3	US-08-482-073-1	Sequence 1, Appli
35	529	3.1	3863	6	5217870-1	Patent No. 5217870
36	528	3.1	1833	1	US-08-365-470-2	Sequence 2, Appli
37	510	3.0	2487	1	US-08-377-292-1	Sequence 1, Appli
38	508	3.0	1848	3	US-09-475-460A-31	Sequence 31, Appli
39	508	3.0	1848	4	US-09-748-061A-31	Sequence 31, Appli
40	508	3.0	1878	2	US-08-435-149-17	Sequence 17, Appli
41	508	3.0	2457	3	US-08-872-157-1	Sequence 1, Appli
42	495	2.9	2457	4	US-09-850-048A-1	Sequence 1, Appli
43	477.5	2.8	4360	6	5378464-1	Patent No. 5378464
44	477.5	2.8	4360	1	US-08-470-350B-1	Sequence 1, Appli
45	447.5	2.6	4182	1	US-08-296-014A-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-911-842A-3
; Sequence 3, Application US/09911842A
; Patent No. 6656707
; GENERAL INFORMATION:
; APPLICANT: Amgen Inc.
; TITLE OF INVENTION: C3B/C4B COMPLEMENT RECEPTOR-LIKE MOLECULUS AND USES THEREOF
; FILE REFERENCE: 01017/37592
; CURRENT APPLICATION NUMBER: US/09/911,842A
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: US 60/222,438
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 11230
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-911-842A-3

Alignment Scores:

Pred. No.:	5,73e-130	Length:	11230
Score:	1852.00	Matches:	808
Percent Similarity:	31.44%	Conservative:	374
Best Local Similarity:	21.49%	Mismatches:	1215
Query Match:	10.90%	Indels:	1363
DB:	4	Gaps:	150

US-10-016-248-2 (1-3104) x US-09-911-842A-3 (1-11230)

Qy	74	CysGrsApPrroGlyIleProGluArgGlyIlyAsrGleugLySerAspPheArg-----	91
Db	1310	TGTCCTCCCTCGAAGCCTCGAAGATGTTTATACAAACACCTTGCAAAACTAC	1369
Oy	92	LengLySerValGlnPheThrCysAsnGluGlyTyraSpLeugInGlySerLyArg	111

Db 1370 TTCAATGCGCGCTGGGGTCCGATGTCGCCGGGCTTTGACCTTGGGAGAGATC 1429
 QY 112 ILethrCysMethylValSerAspMetPheAlaIleProSerAspHisArgProValCys 131
 Db 1430 CATTGTGTCAACC-----AATGTTTGTGTCGTGGACAGAAAGCTTGTGC 1477
 QY 132 ArgAlaArgMetCysAspAlaHisLeuArgGlyProSer---GlyIleIleIleThrSerPro 150
 Db 1478 AGAGTGAAGACGTGC-----CCCACTCCGACAGCCCAACAGCCCACTAGCTGTCC 1534
 QY 151 AsnHepIleGlnIleTyrAspAsnAlaHisCysValTyrIleIleIleAlaLeuAsn 170
 Db 1535 ACTCGGAATAATGCTCTC-----AACACCTGTGT-----TGGTTACCTGC----- 1576
 QY 171 ProSerIleValIleIleValPheGlnIlePheAspLeuAlaArgGlyTyrAspThr 190
 Db 1577 -----AATGAGATACAGATT 1594
 QY 191 LeuThrValGlyAspGlyGlyAspGlyAspGlnIleThrValIleIleIleIleIleIle 210
 Db 1595 -----GAGCGACGACTAGGCTTACTGTCAAGA 1624
 QY 211 AsnAlaCysSerAspSerProHisThrProGlySerArgIleProGlySerMetSerGly 230
 Db 1625 AATGCCAGTGGATGGCCCAAG-----CCCGGTGTGAGAA----- 1663
 QY 231 AspIleTyrArgGlnIleTyrThrValLeuGlnIleCysArgAspIleSerSerSerAsp 250
 Db 1663 ----- 1663
 QY 251 AlaArgSerGlySerValArgIleSerProIleThrSerAsnAlaValGluLeuValAla 270
 Db 1664 ---CGCATTTGTGCGCACTTCAGAACCCCAA----- 1693
 QY 271 ProGlyIleThrGlnIleGlnIleGlnIleSerCysGly---AspProGlyIleProAlaTyrGly 289
 Db 1694 ---GGGCTCATCTTTCTCCACCCAGCTGGCGCAAGAGCCCGCAGGCT----- 1741
 QY 290 ArgArgIleGlnIleSerArgPheHisIleGlyAspThrLeuIlePheGlnIleCysGlnProAla 309
 Db 1742 -----GGATGACCTGTCAAGCTAGCTGCCCGAGGA 1774
 QY 310 PheGluLeuValGlyGlnIleValIleIleThrCysGlnIleAsnAlaGlnIleProSerAlaIle 329
 Db 1775 TACATTTTATCCGGGGTCAAGAGAAGTGAATGTGCCACATCTGGAAAGTGAAGTCCCAA 1834
 QY 330 ---LysProGlyIleCysValPheSerCysPhe----- 338
 Db 1835 GTTCAAGACAGCTGTGTCAAAAGATGTGAGGCTCCCAAAATCAGCTGTCCAAATGACATT 1894
 QY 339 -----PheAsnPheThrSerProSer----- 345
 Db 1895 GAGGCAAAAGATGGGAGCAGACGACTGTCTAATGCCACTGGGCAAGTCCCAACAGCT 1954
 QY 346 -----GlyValValIleuSerProAsnIleProGlyAspTyr----- 357
 Db 1955 AAAGACAACCTGTGTGAAAAGTGTCT-----AGTCCAGCTCCACCCAGCTTTTACCCA 2008
 QY 358 -----GlyAsnHisIleuHisCysValIlePheIleIleLeuAla 369
 Db 2009 CCTTACCTCTTCCCAATTTGAGACGTGGCCATCACTACACGGCAACCACTCATC----- 2064
 QY 369 IaaArgProGluSerArgIleHisIleuAla-PheAsnAspIleAspValGluPro----- 386
 Db 2065 ---CGGTAAACCAAGCAGCTGCACTTTCTATTAAGTCAATTGATGGAACGGCTGTC 2122
 QY 387 -----Gln 387
 Db 2123 ATAGATTGTGCGGATCTCCACTCAATTCAGAGTGTAGAGAGAGAGACCTTCGACAGC 2182
 QY 388 PheAspPheLeuValIleIleIleValIleIleThrAlaGluAlaProValLeuGlyThrPhe 407
 Db 2183 TGGGATGAGGCTCAGTTCTCAGCAACTCGGGGCTGAATTGTTGTCATTACAGCAAGTCAAC 2242

QY 408 Ser---GlyAsnGlnLeuProSerSerIleThrSerSerGlyHisValAlaArgLeuGlu 426
 Db 2243 ACACAAGGGGACATGTTTCTCTCATGGGGAACCGGTGTGTGTGACACAGC----- 2293
 QY 427 PheGlnIleAspHisSerThrGlyIleAspGlyPheAsnIleIleThrPheThrPheArg 446
 Db 2294 -----ACTGACCCCTCAGGCAACACAGACCTGTGACATC---CACATTGCTATAAA 2344
 QY 447 HisAsnGluCysProAspProGlyValProValAsnGlyIleAspPheGlyAspSerLeu 466
 Db 2345 GGTTCCTCCGTGAGAGTCCCTTCAACCCCTGTAAACGGGACTTTATCTGTGCCAGAT 2404
 QY 467 GlnLeuGlySerSerIleSerPheLeuCysAspGlnIlePheLeuGlyThrGlnIleSer 486
 Db 2405 AGTCTGAGATTACTGTGAGCTGTGAGCTGCAAGAGGCTATGATTTCACAGAAAGGTCA 2464
 QY 487 ---GluThrIleThrCysValLeuIleuArgGlyIle-----SerValVal 499
 Db 2465 CCTGAGAAATACTACTGTCTTTGAAAGATGATGTGAGACACCAATACTTACAGAA 2524
 QY 500 TyrAsnSerAlaValLeuArgCysGlnAlaProCysGlyIle----- 512
 Db 2525 TGGCCAGACTGTGCTATAAACGTTTGCAAACATGTTTCAAGTCTTGAATGCTA 2584
 QY 513 -----GlyHisLeuThrSerProSerGly 520
 Db 2585 TACAAACACACTCGCTGTGATGACATGATCTGTTAAGAACTTTTGCACACATTGAG 2644
 QY 521 ThrIleLeuSerProGlyTyrProGlyPheTyrIleAspAla----- 534
 Db 2645 ACTACCTGGGAAACATGTGCTCCGTCCTTTGTAAAGATGATGATGACATTCAGTCAGA 2704
 QY 535 -----LeuSerCysAlaTyrValIleGlnAlaGlnProGlyTyrPro----- 548
 Db 2705 CTGGAGAACCTGACCAAAAATATCATGATGATTAATACACTATGAAAATGCTTT 2764
 QY 549 -----IleIleIleThrPheAspArgPhe 556
 Db 2765 GCATTTGACACGAGGAGCTGGGCTGCAGGCAACAGCTGTGATTAATCTTACATCACTTC 2824
 QY 557 LysThrGlnValAsnTyrAspThrLeuGlnValArgAspArgIleArg----- 571
 Db 2825 CTGATGTGTATCAGAAACACCAACGATGTGGCAAGCCAGATTCGACAGATTAA 2884
 QY 572 -----ThrTyrSerAla 575
 Db 2885 AGAAGTGTCCATTGTGTGACCCCAAAATTCAGTAATTTTAAATCAACAGCTAGCGTG 2944
 QY 576 ProLeuIleGlyValTyrHisGlyThr-----GlnValProGlnPheLeuIleSer 592
 Db 2945 CCACCTCCAGAGAAAGAAACATACCTCTTAATTTGAGAAATCAGACAGCACTCATTAAG 3004
 QY 593 Thr-----SerAsnTyrIleuTyrIleuLeuPheSerThrAspIleSerHisSer 608
 Db 3005 ACATTGAAACAATACCAATGCTGTAAGAAAGACCTTGAAATTAAGAGCCCATGTATTCT 3064
 QY 609 AspIleGlyPheGlnLeuArgTyrGlnIleIleThrLeuGlnIleSerAspHisCys----- 626
 Db 3065 -----TTCACCTGCTCGGAAACAGTGTGCTGACAGCAATTCCTCGAACA 3115
 QY 627 -----LeuAspProGlyIleProValAsnGlyGlnArg----- 637
 Db 3116 GAAAGGCTTTCTCTTGTGACAGACAGGCTGTGCTGAGAGGGGCGCATGTGTCAAC 3175
 QY 638 -----HisGlyAsnAspPheTyrValGlyAlaLeuValThrPheSerCysAspSerGly 655
 Db 3176 TGGCCCTGGGAAACCTTACTCTGTGAGCATTCACCTGTGAAGAGTGCCTCATGGGA 3235
 QY 656 TyrThrIleuSerAspGlyGluProLeuGluCysGlu-----Pro 668
 Db 3236 TCTTACCAAGATGAAGAGGCGAGCTGTAATGCAAGCTGTGTCCCCCAAGGATTCACGCG 3295

Qy 669 AsnPhelInTrpSerArgAlaLeuProSerCysGluAlaLeuCysGlyGlyPheIleGln 688
 Db 3296 GAATACCTCCATTCAGAAAGAGCTCTGAAATGCAAAAGCTCAAGTTAAGCAAGCACTAC 3355
 Qy 689 GlySerSergly 692
 Db 3356 TCTTCAGTGGGTGAGACCTGCAATCTGTCCGTGGTACTTATCAACCGAAATT 3415
 Qy 693 -----ThrIle----- 694
 Db 3416 GGATCCGAGAGCTCTCTATGCCAGAAACACCAACGAGTGAAGAAGAGCCGTG 3475
 Qy 695 -----LeuSer 696
 Db 3476 GACATCTCTGCTTGAGAGTCCCTGCCAGTAGAGAAATTCCTCCGTTCTGGCTAACA 3535
 Qy 697 ProGlyPhePro-----AspPheTyrProAsnAsn-----Leu 707
 Db 3536 CCTGTACACCTTCCCTCGAGACATATTAACCAACCAATGAGGGAAGTCTTCTGCTC 3595
 Qy 708 AsnCySerThrTrp----- 711
 Db 3596 GCTTGCTCCTTTATGAACTACATCACTGCGCCAGCTCCATCAGACTGCTCA 3655
 Qy 712 -----IleIleGluThrSer 716
 Db 3656 AGTTTAGCTCTACTTCTCTCAGACAGCAAGAAAGCATAGTCCCTCTGTCGCTCGA 3715
 Qy 717 HisGlyLeuGlyValPhe-----PheThrPheHisThrPheHisIleu----- 730
 Db 3716 CATTCGCAAGAACATGACAGAGTCAAGCTCTTTCACGAATGCTCTTAAACCC 3775
 Qy 731 -----GluSerGlyHisAspTyrLeuLeuIleThrGluAsn 742
 Db 3776 TGCACAACAGTGAACCTGCCAACAGCTTGCGGTATGTCTCTCTGCCCACT 3835
 Qy 743 GlySerPheThrGlnProLeuArgGlnLeuThrGly----- 754
 Db 3836 GGA-----TACACAGGCTTAAAGTGAAGAGATATTGAT 3871
 Qy 755 -----SerArgLeuProAlaProIleSerAlaGlyLeu-----TyrGlyAsn 768
 Db 3872 GAATGACAGCTCTCTGCTTGC-----CTCAATGTGGAATTTAGAGACCAAGTTGGGGA 3928
 Qy 769 PheThrAlaGlnValArgPhe----- 775
 Db 3929 TTACAGTCGCAATGTTCATTGGGCTATTCAAGTCAAAATATGTGAAGAAATATAATGAG 3988
 Qy 776 -----IleSerAspPheSerMetSerTyr--- 783
 Db 3989 TGTATCTCCAGCCCTTGCTTAAATAAAGAACTGCACTGACGCGCTTGCCAGACTACCC 4048
 Qy 784 -----GluGlyPheAsnIleThrPheSerGluTyrAspLeuGluProCysGlu 799
 Db 4049 TGTACGTGTGGAAGATACATGGGTGTGCACTGTGAACAAGCTCAATGAATGACAG 4108
 Qy 800 GluProGluValProAlaTyrSerIleArgGlyGlyLeuGlnPheGlyValGlyAspThr 819
 Db 4109 TCAAGCCCTGCTTAAACCAAGCAGATTGTGAAGCCAAAGTTGGGGG----- 4156
 Qy 820 LeuThrPheSerCys-----PheProGlyTyrArgLeuGluGlyThrAla 834
 Db 4157 -----TCTCTGTGCAATGCCCAACCGGATTTTGGTACTCGGTGGAAGAAATGTG 4210
 Qy 835 -----ArgIleThrCysLeuGlyGlyArgArgArg 844
 Db 4211 GATGAGTGTCTCAGTCAAGCAATGCCAAATGAGAGCACTGTGAAGATGGTCCAAACGC 4270
 Qy 845 LeuThrPheSerProLeuProArgCysValAlaGluCysGlyAsnSerValThrGlyThr 864
 Db 4271 TTC-----AGGTGT-----CAATGTCCAGCAGGCTTACAGGGGACA 4306
 Qy 865 GlnGlyThrLeuLeuSerProAsnPheProValAsnTyrAsn----- 878

Db 4307 CACTGTGAACGTG-----AACATCAACGAGTGTCACTCAACCCG 4345
 Qy 879 -----AsnAsnHisGluCysIle-----TyrSerIleGlnThrGlnPro 891
 Db 4346 TGTAGAAACAGGCGCACCTGTGTGATGAACATAACTCATACAGTTGTAATGTACCCA 4405
 Qy 892 GlyLeuSerGlyIleGlnLeuValArgAlaPheGluLeuSerGluGlyAspValLeuIys 911
 Db 4406 GGA-----TTTTCAGGCCACAGGTGTGAGACAGAACGCT----- 4441
 Qy 912 ValTyrAspGlyAsnAsnAsnSerAlaArgLeuLeuGlyValPheSerHisSerGluMet 931
 Db 4442 -----TCCGGTTTAACTCGAATTTGAAGTTTCTGCACTTACCGGTACGCTGCTA 4495
 Qy 932 MetGlyVal-----ThrLeuAsnSerThrSerSerSerLeuThrPleu-----Asp 946
 Db 4496 GATGAGATGTGTCCCAACCTTCATGCCGTAACCTGCGCATCTTGATGAATACTCTGAT 4555
 Qy 947 PheIleThr-----AspAlaGluAsnThr--- 954
 Db 4556 GTCATCAACTACGGAGCCCATCTCTATGCACTTGAAGATGACAAAGACACACCTTC 4615
 Qy 955 -----SerLeuGlyPheGluLeuHisPheSerSerPheGluLeuIle----- 968
 Db 4616 CTCTGACTGATTAACAAGGCTGGTCTTATGTGAATGGAAGAAAGATCACCAAC 4675
 Qy 968 ----- 968
 Db 4676 TGCCCTCGTAAATGATGCAATTTGGCATATATTCATACATGAGCAAGATTATGCT 4735
 Qy 969 -----LysCysGluAspProGlyThr----- 975
 Db 4736 GAGCCTGAGAGGCTCTATATAGATGGGAAATATATCTGACGGTGTACTGGCTTCATT 4795
 Qy 975 ----- 975
 Db 4796 GCGAAAGCATTACTGTGGGGGTGATTAAGTTTGGGCAAGACAAAGAAAGAAAGGA 4855
 Qy 975 ----- 975
 Db 4856 GAGGGATTCAACCGCGTGAAGTCTTTGGGCTCCATTAAGCCAGCTCAACTCTGGGAC 4915
 Qy 975 ----- 975
 Db 4916 TATGTCTGTCTCCACAGCAGTGAAGTGTGTGCCAGCTCTGCCAGAGAACTGAGT 4975
 Qy 976 -----ProLysPhe-----GlyTyrLysVal 982
 Db 4976 CGGGGAACGTGTAGCATGGCCGATTTCTGTGGGAAATCACGGGGAAGTGAAGTT 5035
 Qy 983 HisAspGluGlyHisPheAla----- 989
 Db 5036 GATTCAGACAGCATGTTCTCTCTGATTCGCTTGAAGAGATCCGTCCTCACCTG 5095
 Qy 990 -----GlySerSerValSerPheSerCysAspProGly 1000
 Db 5096 AGACCTCATCAGAGAAATCGAAAGCCAGGCTCCAAAGTCAAGTCTGTTGTGAATCGGGC 5155
 Qy 1001 TyrSerLeuArgGlySerGluGluLeuLeuCysLeuSerGlyGluArgArgThrTyrAsp 1020
 Db 5156 TTCAGATGTGTGGAAATCTCTGTCAATATTTGTGAAC-----CAAGGCAATGAGACA 5209
 Qy 1021 ArgProLeuProThrCysVal-----AlaGluCysGly-----GlyThrValArgGly 1036
 Db 5210 CAACCACTCCCGCTCTGAAGCGATTCGCTGTGGGTGCTCCCGCTTGAGAAATGGC 5269
 Qy 1037 GluValSerGlyGlnValLeuSerProGlyTyrProAlaProTyrGlnHisAsnLeuAsn 1056
 Db 5270 TTCTACTACGCGGAGACTTCATCGGGGAGCAGGCTGACCTATACG----- 5317
 Qy 1057 CysIleThrThrIleGluAlaGluAlaGlyCysThrIleGlyLeuHisPheLeuValPhe 1076

[illegible]

QY	1366	ValThrAsnAnPProAArgProValCysThrAlaProCysGlyGlyGlnIleTyrValGlySer	1385
Db	6197	---TGGAAATTCAAAGTAAACCAACCAAGTGGCTGGCT---	6226
QY	1386	AspGlyValValLeuSerProAsnTyrProGlnAsn-----TyrThrSerGlyGlnIle	1403
Db	6227	-----GCTCTCTGTGACGAGACCCCCCAATGTGACCAACGGCTCTCCAGAGCT	6274
QY	1404	CysLeuTyrPheValThrValProLysAspTyrValValPheGlyGlnPheAlaPhePhe	1423
Db	6275	GCT-----GCT-----CACAGGCTCTTTGGAGACACCGCGCTTTTAC	6307
QY	1424	HisThrAlaLeuAsnAspValValGluValHisAspGlyHisSerGlnHisSerArgLeu	1443
Db	6308	TACTGTGG-----GATGGCTACACG-----	6328
QY	1444	LeuSerSerLeuSerGlySerHisThrGlyGluSerLeuProLeuAlaThrSerAsnGln	1463
Db	6329	-----CTGGGCTGATAAATTCACG	6346
QY	1464	ValLeuIleLysPheSerAlaValGlyLeuAlaProAlaArgGlyPheHisPheValIleTyr	1483
Db	6347	CTCATCTGCATATGCCACGGAGACTGGATCCCCCGCGGCG-----	6388
QY	1484	GlnAlaValProArgThrSerAlaThrGlnCysSerSerValProGluProArgTyrGly	1503
Db	6389	CAGGCTGTGCGCGCCGCTGCATAGCTCACTTCTGTGAAAAACCCCATCTGTTCTTACACG	6448
QY	1504	-----LysArgLeuGlySerAspPheSerValGlyAlaIleValArgPheGluCys	1520
Db	6449	ATCTTGGAAATCTGTGACCAAGCAAAAGTTTGCAGCTGGCTCGTAGAGAGCTTCAGATGC	6508
QY	1521	AsnSerGlyTyrAlaLeuGlnGlySerProGlnIleGluCysLeuProValProGlyAla	1540
Db	6509	ATGAGAGGTTTGTGCTGAAACACTTCGCGAAGAGTTAAAGCTTGAGA-----	6566
QY	1541	LeuAlaGlnThrAsnValSerAlaProThrCysValValProCysGlyGlyAsnLeuThr	1560
Db	6557	-----GGTGGAGAGCTGAGC	6571
QY	1561	GlnArgArgGlyThrIleLeuSerProGlyPheProGluProTyrLeuAsnSerLeuAsn	1580
Db	6572	-----CTTCTTCTCCCTC-----TCGGTCCAG	6592
QY	1581	CysValTyrPylValIleValProGluGlyAlaGlyLeuGlnIleGlnValIleSerPhe	1600
Db	6593	TGC-----	6595
QY	1601	ValThrGluGlnAsnThrPheAspSerLeuGlnValPheAspGlyAlaAspAsnThrValThr	1620
Db	6595	-----	6595
QY	1621	MetLeuGlySerPheSerGlyThrThrValProAlaLeuLeuAsnSerThrSerAsnGln	1640
Db	6596	-----ATCCCGGTC-----	6604
QY	1641	LeuTyrLeuHisPheTyrSerAspIleSerValSerAlaAlaGlyPheHisLeuGluTyr	1660
Db	6604	-----	6604
QY	1661	LysThrValGlyLeuSerSerCysProGluProAlaValProSerAsnGlyValLysThr	1680
Db	6605	-----CGATCGGAGACCTCCCAAGCATTCGCAATGGCTACCCGAGT	6646
QY	1681	GlyGlyLysArgTyrLeuValAsnAspValValSerPheGlnCysGluProGlyTyrAlaLeu	1700
Db	6647	GGGACAAACATCAAGTTTGGGGCGCGTGGCTTACAGCTGCCACAAGGATTTCTATATC	6706
QY	1701	GlnGlyHisIleAlaHisIleSerCysMetProGlyThrValArgArgTyrAsnTyrProPro	1720
Db	6707	AAAGGGGAGAAAGAGACGCTG-----GAGCGCAACAGACAGTGGAGTAAACACG	6760

QY 1721 ProLeuCy51lealaglnCy5glYThrValgluGluMetGluGlyValIleLeuSer 1740
 |||
 DB 6761 CCCACTGCG----- 6769
 QY 1741 ProGluPheProGluYasnTYrProSerAsnMetAspCy5SerTrpLysIleAlaLeuPro 1760
 |||
 DB 6770 -----CATCCT-----GTGCTCCGTAAAGCGACCACTTAAGGTTAG 6805
 QY 1761 ValGluPheGlyAlaH1leGlnPheLeuAsnPheserThrGluProAsnH1leAspTYr 1780
 |||
 DB 6806 AACGGCTTCTCGAGCAACACCTGGACGACCTTTGAGAGCAAGGAGTTCCAGTCC 6865
 QY 1781 IleGluIleArgAsnGlyProTYrGluThrSerArgMetMetGlyArgPheserGlySer 1800
 |||
 DB 6866 -----AACCCAGGCTATAGGCA-----GCCGGAAGT 6892
 QY 1801 GluLeuProSerSerLeuLeuSerThrSerH1leGluThrValTYrPheH1leSerAsp 1820
 |||
 DB 6893 -----CCTGTGTTGTTGGCAAGCCAAATCGC-----CACTGGACAGCGAG 6934
 QY 1821 HisSerGlnAsnArgProGluPheLysLeuGluTYrGlnAlaTYrGlnLeuGlnGlyCys 1840
 |||
 DB 6935 GCCCTCTGCTCGACCCCTCTC-----AACTGT 6964
 QY 1841 ProAspProGluProPheAlaAsnGlyIleValArgGlyAlaGlyTYrAsnValGlyGln 1860
 |||
 DB 6965 GGGAAACCCCTCCATTCAGAAATGCGCTTTTGAAGAGAAACCTTGAAGTGGGCTC 7024
 QY 1861 SerValThrPheGluCysLeuProGlyTYrGlnLeuThrGlyH1leProValLeuThrCys 1880
 |||
 DB 7025 AAGGTCAGTTGTCGTAAATGAGGATATGAGCTCGTGGTGAATATTCCTGGACTTGC 7084
 QY 1881 GlnH1leGlyThrAsnArgAsnTrpAsp---HisProLeuProLysCy5GluValPro--- 1898
 |||
 DB 7085 CAG-----AAATCGCAAAATGGAGTAAAGCAAGCCGAAAGT---GTCCCAACC 7135
 QY 1899 ---Cy5GlyGlyAsnIleThrSerSerAsnGlyThrValTYrSerProGlyPheProSer 1917
 |||
 DB 7136 AAGGTGCAGAGCTCTCTTGAAGAAACAGCTCGATTTGAAGAA----- 7183
 QY 1918 ProTYrSerSerSerGlnAspCy5ValTrpLeuIleThrValProIleGlyH1leGlyVal 1937
 |||
 DB 7184 -----TTAGCTCCGAGTGAAGTATGATGACATTCCTGTAAAGAGGCGATGCTTG 7237
 QY 1938 ArgLeuAsnLeuSerLeuLeuGlnThrGluProSerGlyAspPheIleThrTrpAsp 1957
 |||
 DB 7238 CAA---GCCCCCTCTGTCTGAAGTCTTGCCATCCGGCA-----TGAAGT 7282
 QY 1958 GlyProGlnGlnThrAlaProArgLeuGlyValPheThrArgSerMetAlaLysLysThr 1977
 |||
 DB 7283 GGT----- 7285
 QY 1978 ValGlnSerSerSerAsnGlnValLeuLeuLysPheH1leArgAspAlaAlaThrGlyGly 1997
 |||
 DB 7285 ----- 7285
 QY 1998 IlePheAlaIleAlaPheSerAlaTYrProLeuThrLys-----Cy5ProProPro 2014
 |||
 DB 7286 -----TCCCTTCCTAATTTGTAGATGTCCTTGTTCCTCCCTCCCTC 7324
 QY 2015 ThrIleLeuProAsnAlaGluValValThrGluAsnGluGluPheAsnIleGlyAspIle 2034
 |||
 DB 7325 CCCTTGATCCCTTCGGC---GTCCCTGCGCTTCCGGGTCTTTCATTTTGGAGTACT 7381
 QY 2035 ValArgTYrArgCy5LeuProGlyPheThrLeuValGlyAsnGluIleLeuThrCysLys 2054
 |||
 DB 7382 GTCAAGATCTGCTGTGTCGAGGGTTTTTCTTAAGAGGACGTCAACATCTCTGCGAG 7441
 QY 2055 LeuGlyThrTYrLeuGlnPheGluGlyProProProIleCys---GluValH1leCy5Pro 2073
 |||
 DB 7442 GCTGATAGC-----ACCTGGAAGTTCTCAATGGCCGAATGCGTTCGAGTAAATGTCGCC 7495
 QY 2074 ThrAsnGluLeuLeuThrAspSerThrGlyValIleLeuSerGlnSerTYrProGlySer 2093

DB 7496 CAACCTGAGAGATCCTCAAC-----GGATCATCCACGTACAGAGGCTTGCTATCTC 7549
 QY 2094 TYrProGlnPheGlnThrCy5SerTrpLeuValArgValGluProAspTYrAsnIleSer 2113
 |||
 DB 7550 AGACCAACGCTCTACACTCTC-----AAGCCAGGCTTTGAGTTA--- 7588
 QY 2114 LeuThrValGluTYrPheLeuSerGluLysGlnTYrAspGluPheGluIlePheAspGly 2133
 |||
 DB 7589 -----GTGGGCAATGCTACACCTCTGCGG 7615
 QY 2134 ProSerGlyGln-----SerProLeuLeuLysAlaLeuSerGlyAsnTYrSer 2149
 |||
 DB 7616 GAAATGCGCAGTGGCTCGAGGAAACCAATGCAAAACCAATTGA----- 7663
 QY 2150 AlaProLeuIleValThrSerSerSerAsnSerValTYrLeuArgTrpSerSerAspH1s 2169
 |||
 DB 7663 ----- 7663
 QY 2170 AlaTYrAsnArgLysGlyPheLysIleArgTYrSerAlaProTYrCy5SerLeuProArg 2189
 |||
 DB 7664 -----TCCCAAGGCCAAG 7678
 QY 2190 AlaProLeuH1leGlyPheIleLeuGlyGlnThrSerThrGlnProGlyGlySerIleH1s 2209
 |||
 DB 7679 GAGATTTTAATAGC---CAATTCCTCCGTGAGCTTTCAGTATGAGCAAAACATACACA 7735
 QY 2210 PheGlyCy5AsnAlaGlyTYrArgLeuValGlyH1leSerMetAlaIleCy5ThrArgH1s 2229
 |||
 DB 7736 TACTTTGTATCCGGGGCTTCCGGCTCGAAGGTCCCAATCCCTGACCTTTTGAAGACA 7795
 QY 2230 ProGlnGlyTYrH1leLeuTrpSerGluAlaIleProLeuCy5GlnAlaLeuSerCy5Gly 2249
 |||
 DB 7796 GGTGAC-----TGGATATGAGTCCCTCTTGTATGATCCATCTGACGT 7843
 QY 2250 LeuProGluAlaProLysAsnGlyMetValPheGlyLysGlyTYrThrValGlyThrLys 2269
 |||
 DB 7844 GACCCACAGCCCAATTGAATGTTGTGTGAAGGTGCGGATTAACAATCGGCGCATG 7903
 QY 2270 AlaValTYrSerCy5SerGlyGlyTYrH1leLeuGlnAlaGlyAlaGlyAlaThrAlaGlu 2289
 |||
 DB 7904 ATCATTAATAGCTGCTTCCCTGGGTTTCAGGTGTTGTGTCATGCCAGCAGACC----- 7957
 QY 2290 Cy5LeuAspThrGlyLeuTrpSerAsnArgAsnValProProGlnCy5ValProValThr 2309
 |||
 DB 7958 TGTGAAGATCGGGA---TGTCAAGCTCCAGC---CCAACTGTGTAACCATAGAC 8008
 QY 2310 Cys-----ProAspVal-----SerSerIleSerValGluH1leGlyArgTrp 2323
 |||
 DB 8009 TCGGCTCCCTCTCTCAATAGACTTTGGTACGTACTTAAGTCAAGATGCGCAGAGGA 8068
 QY 2324 ArgLeuIlePheGlu----- 2328
 DB 8069 CATTTGATCAAGAAATGACATGATGAGATGCCATATCTGCTCACCTCAACATTTG 8128
 |||
 QY 2329 -----ThrGln 2330
 DB 8129 GAAGCAACAGCTAAGGCTTGAAGAAATACAAGAGTGGCTGCTTCATGATGATCCAC 8188
 QY 2331 TYrGlnPheGlnAlaGlnLeuMetLeuIleCy5AspProGlyTYrTYrTYrThrGlyGln 2350
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 DB 8189 TTCTCTATGCGACAGATGTTTCTCTACAGCTGCGAGCTGTTTATGAACGTGGGAAATC 8248
 QY 2351 ArgValIleArgCy5GlnAlaAsnGlyLysTrpSerLeuGlyAspSerThrProThrCys 2370
 |||
 DB 8249 CCGTGTGCTATCGCCAGAAATGAGTGAAGT-----GTAACCGACCCCTTTCG 8302
 QY 2371 ArgIleIleSerCy5GlyGluLeuProIle---ProProAsnGlyH1leAspGlyThr 2389
 |||
 DB 8303 ATTTCATTAAGT---GATTTGCTGTTGCTCCGAAATGAGCTTTTACATTTCACA 8359
 QY 2390 LeuSerValTYrGlyAlaThrAlaIlePheSerCy5AsnSerGlyTYrThrLeuValGly 2409
 |||

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Qy 2410 SerThrValArgGluCysMetAlaAsnGlyLeuTrpSerGlySerGluValArgCysLeu 2429
Db 8420 TCCCACTTAAGACTGTCTGTGCAGAAATAGACAGTGGAGTGCACCTGTTCCACCTCTGA 8479
Qy 2430 AlGlyHisCysGlyThrProGluProIleValAsnGlyHisIleAsnGlyGluAsnTrp 2449
Db 8480 GCCATCTCATGCAATGAAACCAACCACTCTGGAATGATCCATCAAGAGATGATAC 8539
Qy 2450 SerThrArgGlySerValValTyrGlnCysAsnAlaGlyPheArgLeuIleGlyMetSer 2469
Db 8540 TCCTACCTGGGTGTATAGTACTAGAGTGTACTGTGGCTATATCTCATATGCTCTGAG 8599
Qy 2470 ValArgIleCysGlnGlnAspHisIleTrpSerGlyValTrpThrProPheCysValProIle 2489
Db 8600 AAGAGCATGCAAGAAATAGATGGATGGGATGGAGCCCATGTGTATCTCTGTA 8659
Qy 2490 ThrCysGlyHisProGlyAsnProValAsnGlyLeuThrGlnGlyAsnIlePheAsnLeu 2509
Db 8660 GACTGTGTCTACACCCCAAGTCCCAACCAATGGCCGAGTGAAGAGAAATACACATTTC 8719
Qy 2510 AsnAspValValAlaPheValCysAsnProGlyTyrMetAlaGluGlyAlaAlaArgSer 2529
Db 8720 CAAAGGAGATTAATATCTCTGTGGCGTGAAGGGTTACTGGAAGAGCCAGAGTCTGT 8779
Qy 2530 GlnCysLeuAlaSerGlyGlnTrpSerAspMetLeuProThrCysArgIleIleAsnCys 2549
Db 8780 ATCTGCTTTCATCAATGAGATGAGTGAAGTGCATCCCACTGCACTGCTGTTAAGTGT 8839
Qy 2550 ThrAspProGlyHisIleGlnGluAsnSerValArgGlnValHisIleAsnGlyProHisArg 2569
Db 8840 CTCGCCCAACACAGTGCCTCAATGGGTG-----GCAATGGCCCTAAGAC--- 8884
Qy 2570 PheSerPheGlyThrThrValSerTyrArgCysAsnHisGlyPheTyrLeuGlyThr 2589
Db 8885 TATGGGTTCAGAAAGAAAGATGAGCTTCACTGTCTAGAGGGCTATGTGTCAGGGGGCT 8944
Qy 2590 ProValLeuSerCysGlnGlnGlyAspGlyThrThrAspArgProArgProGlnCysLeuLeu 2609
Db 8945 CCAAGACTCACTGTCAGTCCCAATGAGGACTGGAGTGAAGACAGAGTCCCTGCTTAACCA 9004
Qy 2610 ValSerCysGlyHisProGlySerProProHisIleSerGlnMetSerGlyAspSerTyrThr 2629
Db 9005 GCATCCTGTGTCTCTCTCTGCGCAACCTTCCCAAGGCTCTCCCTTAATGCTTTTAT 9064
Qy 2630 ValGlyAlaValAlaValArgTyrSerCysIleGlyValArgThrLeuValGlyAsnSerThr 2649
Db 9065 CATGGGGGACCATACATGATCTAGTGTCTTACTGTTATTAAGCTTCATGGAACCATCA 9124
Qy 2650 ArgMetCysGlyLeuAspGlyHisIleTrpThrGlySerLeuProHisCys----- 2665
Db 9125 AGAAGATGCTTCTCCCAATGATGCTCTGAGCGCAAGCTCGCATCTGCTTCACTTGCAG 9184
Qy 2666 -----SerGlyThrSerValGlyVal----- 2672
Db 9185 TGTTCACACCCATCATTTCAACAGGAAACATCAAGCAACTGATTTGGATGTGAAG 9244
Qy 2672 ----- 2672
Db 9245 ACGGTCAGATGATGCTTCAAGAGCTTCAAGCTGCTTGAATTTCTGAATCACCTGT 9304
Qy 2673 -----CysGlyAsp----- 2675
Db 9305 GATGCCAATGGCAATGCTGTGACGTCCACTGTGTGAGCAGCTCAAGTGGGGCTCTTC 9364
Qy 2676 ProGlyIleProAlaHisGlyIleArgLeuGlyAspSerPheAspProGlyThrValMet 2695
Db 9365 CCAACCATATCC---AAGCAATTTGCTCTTGAAGGCAAGCTTTCGAGAGCAATGTGTGA 9421
Qy 2696 ArgPheSerCysGlyAlaGlyHisIleValLeuArgGlySerSerGlyIleArgThrCysGlnAla 2715
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Qy 2716 AsnGlySerTrpSerGlySerGlnProGluCysGlyValIleSerCysGlyAsnProGly 2735
Db 9482 AAGCAATATGAGCGCAAGCTTACCCACACGATGTGAACCCCTGTCTGTGACCCCAACA 9541
Qy 2736 ThrProSerAsnAla----- 2740
Db 9542 ACTGTAGCCAAATGCACTGGCAACAGAGAGGCTCATCTATGAAGCAAGTGAATCTC 9601
Qy 2740 ----- 2740
Db 9602 AGGTGCTGAAGGATATGTGATGATTCGATACATACATTCACCTGCCAGCAAGAT 9661
Qy 2740 ----- 2740
Db 9662 GGCCATGGGTCCCTGAAGAAATCACTGCACTGCTTAAAAATGCCCTGTCCATCCAAC 9721
Qy 2741 -----ArgValAlaPhe-----SerAspGlyLeuValPheSerSerIleValTyrGlu 2757
Db 9722 ATGACACGATACGTTTTCACGAGATGACTTCCAGTGAACAGACAAAGTTTCTGTCTCA 9781
Qy 2758 CysArgGluGlyTyrTyrAlaThrGlyLeuLeuSerArgHisCysSerValAsnGlyThr 2777
Db 9782 TGTGCAGAAAGGTTTAAACCAAGAGAGTGAATCTGGTCAACATGCCAGCCGAGTACA 9841
Qy 2778 TrpThrGly-----SerAspProGluCysLeuValIleAsnCysGlyAspProGlyIle 2795
Db 9842 TGGAGCCACCATTTTCTGATGAATCTGTATCCAGATGTTGTGGGATCTTGAAGC 9901
Qy 2796 ProAlaAsnGlyLeuArgLeuGlyAsnAspPheArgTyrAsnIleThrValThrTyrGln 2815
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Qy 2816 CysValProGlyTyrMetMetLeuSerHisArgValSerValLeuSerCysThrIleAsp 2835
Db 9962 TGTGACCTCGCTACAAATTAAGAGGGAAACAGAGAACGATC-----TGCCAGAGAAAC 10015
Qy 2836 ArgTrpTrpAsnGlyThrIleAspProValCysValAlaLeuMetCysValProProLeu 2855
Db 10016 AACAAGTGAAGTGAAGAGTGTGCAAGTGTGCAAGAAACATATGTAGCTCCAGCTGAG 10075
Qy 2856 IleProAsnGlyValValAlaGlySerAspPheMetTrpGlySerSerValThrTyrAla 2875
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Qy 2876 CysLeuGluGlyTyrGlnLeuSerLeuProAlaValPheThrCysGluGlyAsnGlySer 2895
Db 10136 TGTCAAGAGGCTACACCTGGAAGGGTCCCCGAGGACACACTGCACTGCAATGGAAC 10195
Qy 2896 TrpThrGlyGluLeuProGlnCysPheProValPheCysGlyAspProGlyVal---Pro 2914
Db 10196 TGAATACCTGACTTCCCTCTGCAACCAATTCATGATCCCTGCTCTTTGTGATTTCT 10255
Qy 2915 SerArgGlyArgArgIleAspArgGlyPheSerTyrArgSerSerValSerPheSerCys 2934
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Qy 2935 HisProProLeuValLeuValGlySerProArgArgPheCysGlnSerAspGlyThrTrp 2954
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Qy 2955 SerGlyThrGlnProSerCysIleAspProThrIleuThrThrCysAlaAspProGlyVal 2974
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Qy 2975 ProGlnPheGlyIleGlnAsnAsnSerGlnGlyTyrGlnValGlySerThrValLeuPhe 2994
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Qy 2995 ArgCysGlnLeuGlyTyrLeuLeuGlnGlySerThrThrArgThrCysLeuProAsnLeu 3014
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QY 520 ----- 520
 Db 2411 GAGATGTTCAAAAGACGCTGTTGATGACAGATCTGATGAAGAATTCTGAA 2470
 QY 521 -----ThrlleuserProglYlTrpProglYpHeTyrlsAspAla----- 534
 Db 2471 GCATTGAGACGACCTGGAAAAATGTCCTCATCTTTGTAGTATGATGACAGAGCATT 2530
 QY 535 -----LeuserCybalTrpValIleGluIleaglInProglYlYr 547
 Db 2531 GACTGAGACTGGAGAGAACTGACCAAAAATATTGGCTAGAAATATATATGACTAT 2590
 QY 548 Pro-----IleuYslleThr 552
 Db 2591 GAAATGGCTTTCGCAATTGGACCAAGTGGCTGGGGTGCAGCTAATAGCTGATTCCT 2650
 QY 553 PheAspArpPheLeuYslTrpGluValIleAsnYrAspThrLeuGluValAlaArgAspGlyArg-- 571
 Db 2651 TAGAGTACCTTCTCGACACTGTGCAAGAAACAGCCAAAGATCGGCAATGCCAAGTCC 2710
 QY 571 ----- 571
 Db 2711 TCACGATTAAGAAAGTCCCATTTATCTGACTATATAATTAAGTTAATTTTAACATC 2770
 QY 572 ThrTySerAlaProleuIleGlyValTyrlsGlyThr----- 584
 Db 2771 ACAGCTAGTGTGCTGATTAACCCGATGAAGAAATGATACCTTGAAATGGAAAAATCAGAA 2830
 QY 585 GluValProglInPheLeuIleSerThrSerAsnTyrlsLeuTyrlsLeuPheSerThrAsp 604
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 QY 605 LysSerHisSerAspIleGlyPheGluLeuAlaGlyTyrlsThrIle----- 619
 Db 2891 CCCATGATATTC-----TTTCAGCTTGATCAGAAATACTTATAGCCGACAGCAAT 2941
 QY 620 -----ThrlleuGlnSerAspHisCysLeuAspProglYlIleProValIleaglYlGln 636
 Db 2942 TCATTGAAACAAAAAGGCTTCCCTTCTGACAGACAGGCTCAGTGTGAGAGGCGCT 3001
 QY 637 ArgHisGlyAsn-----AspPheTyrlsAlaGlyValAlaLeuValThrPheSerCys 652
 Db 3002 ATGATGTCAATTCCTTGGGAACTATAT-----AATCTGGAACAATTCACCTGT 3055
 QY 653 AspSer-----GlyTyrlsThrLeuSerAspGlyGluProleuGluCysGly-- 667
 Db 3056 GAAAGCTGCCGAGATCGATCTCTATCAAGATGAAGAGGCA--CTTGAGTGCAGCTT 3112
 QY 668 -----ProAsnPheGlnTrpSerArgAlaLeuProSerCysGluVal 681
 Db 3113 TGCCCTCTGGGATGTACAGGAATATATCATTCAGAAACAATCTGTGATTGAAAGCT 3172
 QY 682 LeuCyseGly----- 684
 Db 3173 CAGTGTAAACAAAGCACTATCTATACAGTGAAGCTTGAGATGCTGTCACTG 3232
 QY 685 GlyPheIleGln-----GlySerSerClyThrIleLeuSerPro----- 697
 Db 3233 GGCACCTTATCAGCAAAATTTGGTTCCGAGAGCTGCTCTGTCCAGAAACACCTCA 3292
 QY 698 -----GlyPhePro----- 700
 Db 3293 ACTGTGAAGAGAGAGCGGTGACATTTCTGATGTGAGATTCCTTGTCCAGAGAGAAA 3352
 QY 701 -----AspPheTyrlsProAsnAsn 706
 Db 3353 TTCTGCGCTTGGGTTAATGCTGTCACCCATGCTCTGTCATTAACCAACTAAT 3412
 QY 707 -----LeuAsnCyseThrTrpIleIleGluThrSerHisGlyYlGly 720
 Db 3413 GCAGGAAAGGCTTCTGCTGCTGCTGCTGCTT-----TATGAAACTACC 3457
 QY 721 ValPhePheThrPheHisThrPheHisLeuGlnSerGlyHisAspTyrlsLeuLeuIleThr 740

Db 3458 CCATTGCGGTGTTCCAAATCC-----ATCACCA 3484
 QY 741 GluAsnGlySerPheThrGlnProleuArgGlnLeuThrGlySerArgLeuProAlaPro 760
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 QY 761 IleSerAlaGly----- 764
 Db 3542 GCCTCTTGGACATATTAAAAAGAGCATGAATCAGACGTCAGCTTTCCATGAAATGC 3601
 QY 765 -----LeuTyrlsAsnPheThrAlaGlnVal-----ArgPheIleSer 777
 Db 3602 TTCTTTAACCTTGGCAAAATATGTAACCTGCAGCAACTGGCGCTGTATGTTGT 3661
 QY 778 AspPheSerMetSerTyrlsGluGlyPheAsnIleThrPheSerGluTyrlsAspLeuGluPro 797
 Db 3662 CTGTGTCCACTGGATATACAGGCTTAAAG-----TGTGAAACAGACATCGATGAG 3712
 QY 798 CysGluGluProGluValProAlaTyrlsSerIleArgIleGlyLeuGlnPheGlyValGly 817
 Db 3713 TGCAGC-----CCACTGCTTGCCTCAACATGAGAGTTGTAAAGACTAGT 3760
 QY 818 AspThrIleuThrPheSerCysPheProglYlYrArg----- 829
 Db 3761 GGGAAATTCATTTGTAGAGTCCCATCAGTTTACACAGGTCAAGCGGTGTGAAAGAAATATA 3820
 QY 830 -----LeuGluGlyThrAla-- 834
 Db 3821 AATGAGTGTAGCTCAGTCTTGTTTAAATGAAGAAATCTGTGTTAGTGTGCTGGC 3880
 QY 835 ---ArgIleThrCysLeuGlyGly-----ArgAlaArg 844
 Db 3881 TATCGTTGACATGtGTGAAGAGATTGTAGGCTGATGTAAGAACAGAACTCAATGA 3940
 QY 845 LeuTrpSerPro----- 849
 Db 3941 TCCAGTCAAMCCCATGCTTAATATGATGATGATGATGAAAGCAGTTGGGGAAATCTTG 4000
 QY 850 -----LeuProArgCysVal 854
 Db 4001 TGCAAATGCCCACTCGATTTTGGGTACCCGATGTGAAAGAAAGATGATGATGCTATAT 4060
 QY 855 AlaGlu---CysGlyAsnSerValThrGlyThrGlnGlyThr-----Leu 868
 Db 4061 AGTCAGCCTATGAAAAATGAGACTACCTGTAAAGAGCGGTGCCAATATGCTCAGATGCCGTG 4120
 QY 865 LeuSerProAsnPhe-----ProValAsnTyrlsAsn----- 878
 Db 4121 TGTGAGCTGGCTTACAGAGATCACACTGTGAATGAAATGAAATGATGATGCTATAT 4180
 QY 879 -----AsnAsnHisGlyCysIle-----TyrlsIleGlnThrGln 890
 Db 4181 CCATGTGAATAACAGGCCACCTGTGTGATGTAATTAATTCATACAGTTGTAAGTCTAG 4240
 QY 891 ProGly-----LysGlyYlIleGlnLeuYsAla 899
 Db 4241 CAGGATTTTACAGCAAAAGTGTGAAACAGAACAGCTTACAGGCTTTAACTGGAT-- 4297
 QY 900 ArgAlaPheGluLeuSer----- 905
 Db 4298 -----TTTGAAGTTTCTGGCATTTATGATATGTCATGCTAGATGCGATGCTCCATCT 4351
 QY 905 ----- 905
 Db 4352 CTCGATGCTTAACCTGTACTTGTGATGAATCTGTGAGCAATGAATATGGAACA 4411
 QY 906 -----Glu 906
 Db 4412 CCAATCTCTAAGAGTGTGATGAACGAGCAAGAAATACCTTGTCTGTGATTAATAC 4471
 QY 907 GlyAspValLeu----- 910

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Db 4472 GGCTGGGCTTTATGATGATGCGAGGAAAGATACAACTGTCCTCGTGATGAT 4531
Qy 911 -----LysVal.Tyr 913
Db 4532 GGCAGATGCAATATTGCAATCACTTGACAAGTCCAAATGGCAATCTGGAAGTCTAT 4591
Qy 914 -----Asp1.Yasn-----Asn 917
Db 4592 ATGATGGGAAATTATCTGACGGTGGTCCCTCTCTGTGGTTGCCATACCTGCT 4651
Qy 918 AsnSer1AarGluLeuGlyVal-----PheSerHisSer 929
Db 4652 GGTGTCGCTTATCTGGGGCAAGACAAAGAGAGAGAGGATTCAGCCCACT 4711
Qy 930 GluMetSerGlyValThrLeuAsnSerThrSerSerSerLeuThrPheAspPheIleThr 949
Db 4712 GAGCTTTTGTGGCTCATAGACCACTC-----AACCTCTGG-----GACTATGTCCTG 4762
Qy 950 Asp-----AlaGluAsnThrSerLeuGlyPhe 958
Db 4763 TCTCCACAGCAGTGAAGTCACTGGCTACCTCTCTCCACAGGAATCAGTAAAGAAAC 4822
Qy 959 GluLeuHisPheSerSerPhe-----Glu 966
Db 4823 GTGTAGACATGGCTGATTTCTTGTGACGAATGCGGAAAGTGAAGATCTTAAG 4882
Qy 967 LeuIleLeuGlySerGluAspProGlyThrProIlePheGly-----TyrLys 981
Db 4883 AGCATATTGTTGTTGAT-----TGCCACAGCTTAAGAGGTCAGTCCATCTAGA 4936
Qy 982 ValHisAspGluGlyHisPheAlaGlySerSerValSerPheSerCysAspProGlyTyr 1001
Db 4937 ACTGCATCTGAAGATTAAAGCCAGGTTCCAAAGTCAATCTGTTGATGTCAGGCTTC 4996
Qy 1002 SerLeuArgGlySerGluGluLeuLeuCysLeuSerGlyGluArgGlyThrTyrAspArg 1021
Db 4997 CAGCTGGCGGGAACCTGTCAGTACTGTCGAT-----CAAGACAGTGAACAA 5050
Qy 1022 ProLeuProThrCysValAlaGluCysGlyGlyThrValArgGlyGluValSerGlyGln 1041
Db 5051 CCACCTCTCTCACTGT-----GAA 5068
Qy 1042 ValLeuSerProGlyTyrProAlaProIleGluHisAsnLeuAsnCysIleThrThrIle 1061
Db 5069 CGCATTAAGCTGTGGGGGCCCACTCTCTTGGAAATGGCTTCCATCA-----GCCGAT 5122
Qy 1062 GluAlaGluAlaGlyCysThrIleGlyLeu-----HisPheLeuValPhe 1076
Db 5123 GACTTCATGCTGCGACAGACAGTAACCTACCAAGTGAACATGCTACTATTTGGGT 5182
Qy 1077 AspThrGluGluValHisAspValLeuArgIleThrAspGlyProValGluSerGlyVal 1096
Db 5183 GACTCAAGAGATGTTCTGTACAGATATAGGAGCTGGAACGGCGTTTCAACCTCTGCTT 5242
Qy 1097 LeuLeuGlySerGluLeuSer----- 1102
Db 5243 GATGTCAATGATGTGCGATTTGATCAGATTGTAGTGAATGCTTCTTGCCTGAACGTA 5302
Qy 1102 ----- 1102
Db 5303 GATGATCTCATATGTTATGTTGTCACACCTACACAGAGATGGGAAAAACTGTGCA 5362
Qy 1103 -----GlyProAlaLeuProIleAspLeuHisSerThrPheAsnSer 1116
Db 5363 GAACCTATAAATGTAAAGCTCCAGAAATCCGAAATGCGCACTCTCA-----GCTGAG 5419
Qy 1117 ValValLeuGlnPheSerThrAspPhePheThrSerIleGlnIleAlaIleGln--- 1135
Db 5420 ATTATATACAGTAGGTGCCGAATTCATTTTGTGTGAGGAAGATCCAGTTATGGGA 5479
Qy 1136 -----PheSerValSerThr 1140
Db 5480 GTAAACAATAATCAGATGTTGGAGTCTGGAATGAATCATCTAATACCATATTGTAAA 5539

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Qy 1141 AlaThrSerCysAsnAspProGlyIleProGluAsnGlySerArgSerGlyAspSerThr 1160
Db 5540 GCTGTTTCAATGTTGTTAAACCGGCTATCCAGAAATGTTGATTCATTCAGGACTTATTC 5599
Qy 1161 GluAlaGlyAspSerThrValPheGlnCysAspProGlyTyrAlaLeuGlnGlySerAla 1180
Db 5600 ACTTTTGGCAGCAAGAGACATATAGGTGTAATAAGATATATCTGCGCCGGTGAATAA 5659
Qy 1181 GluIleSerCysValIleValIleGluAsnArgPhePheThrGlnProSerProProThrCys 1200
Db 5660 GAATCATCTGCTGTTGTAACAGTTCT-----TGAGTCAATTCCTCCCTGCTGTGT 5710
Qy 1201 IleAlaProCysGlyGlyAspLeuThrGlyProSerGlyValIleLeuSerProAsnThr 1220
Db 5710 ----- 5710
Qy 1221 ProGluProTyrProProGlyIleGluCysAspThrIleValSerProAspTyr 1240
Db 5711 -----GAAACCACTG-----AAGTGTCT-----AGTCCGGA--- 5737
Qy 1241 ValIleAlaLeuValPheAsnIlePheAsnLeuGluProGlyTyrAspPheLeuHisIle 1260
Db 5738 -----AATATAATATATGA-----AATATATT 5761
Qy 1261 TyrAspGlyArgAspSerLeuSerProLeuIleGlySerPhe-----TyrGlySer 1277
Db 5762 TTGAGTGGGCTTCACTCACTTTCTACTGATCATATTACAGCATACAGATTAACGTTA 5821
Qy 1278 GluLeuProGlyArgIleGluSerSerAsnSerLeuPheLeuAlaPheArgSerAsp 1297
Db 5822 CAGGGCCCTTCATATTATGATGACCGCTTCGGCATCTGG-----GAC 5866
Qy 1298 AlaSerValSerAsnAlaGlyPheValIleAspTyrThrGluAsnProArgGluSerCys 1317
Db 5867 AGAGCCGCCACCTGCTGCTGCTGCTGCTC-----TGT 5899
Qy 1318 PheAspProGlySerIleLeuAsnGlyThrArgValGlySerAspLeuLeuGlySer 1337
Db 5900 GGAGAACCACTCCATCAAAAGATGCTGATTAACGGGAATTAACCTTCCATTCAGAAC 5959
Qy 1338 SerValThrTyrTyrCysHisGlyGlyTyrGluValGluGlyThrSerThrLeuSerCys 1357
Db 5960 ACCGTCACTTACACTTGCAAGAAAGCTATATCTTCTGCTGCTGACACATTAAGATGC 6019
Qy 1358 IleLeuGlyProAspGlyIleProValTyrAsnAsnProArgProValCysThrAlaPro 1377
Db 6020 CTG-----GCCAGCGCAAG-----TGAGATGAAGTGAACAGCAGTGCCTGGCT--- 6064
Qy 1378 CysGlyGlyGlnTyrValGlySerAspGlyValValLeuSerProAsnTyrProGln--- 1396
Db 6065 -----GTCCTCTGTGATGAGCCACCATT 6088
Qy 1397 ---AsnTyrThrSerGlyGlnIleCysLeuTyrPheValThrValProIleAspTyrVal 1415
Db 6089 GTGGACCAACCTCTCCAGAGACTGCC-----CATCGG 6121
Qy 1416 ValPheGlyGlnPheAlaPhePheHisThrAlaLeuAsnAspValValGluValHisAsp 1435
Db 6122 CTCTTGGAGACATTTGATCTACTACTGCTCT-----GAT 6157
Qy 1436 GlyHisSerGlnHisSerArgLeuLeuSerSerLeuSerIleSerHisThrGlyGluSer 1455
Db 6158 GGTTAACAGC----- 6166
Qy 1456 LeuProLeuAlaThrSerAsnGlnValLeuIleLysPheSerAlaLysGlyLeuAlaPro 1475
Db 6167 -----CTAGCAACAATTCACGCTTCTTGCAATGCCAGGCAAGTGGATACCCCA 6220
Qy 1476 AlaArgGlyPheHisPheValTyrGlnAlaValProArgThrSerAlaThrGlnCysSer 1495
Db 6221 GAAGGT-----CAAGACATGCCCGTGTGTATGATCATTTCTGTGAA 6262

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Db 6263 AAACCCCATCGCTTCCCTATAGCATCTTGATCTGTGAGCAAAATTGCACT 6332
QY 1513 GlyAlaIleValArgPheGlnCysAsnSerGlyTyrAlaLeuGlnGlySerProGluIle 1532
Db 6323 GCGTCAGTTGAGGCTTTAAATGATGAAAGCCTTGTACTGAACACTCAGCAAAAGATT 6382
QY 1533 GlnCysLeuProValProGlyAlaLeuAlaGlnTTPaenValSerAlaProThrCysVal 1552
Db 6383 GAATGATG-----AGAGGTGGCGAGTGGAAAC----- 6409
QY 1553 ValProCysGlyGlyAsnLeuThrGlnArgArgGlyThrIleLeuSerProGlyPhePro 1572
Db 6410 -----CTT 6412
QY 1573 GluProTyrLeuAsnSerLeuAsnCysValTrrpLysIleValValProGluGlyAlaGly 1592
Db 6413 TCCCCCATG-----TCCATCCAGTGC----- 6433
QY 1593 IleGlnIleGlnValIleValSerPheValThrGlnGlnAenTrrpAspSerLeuGluValPhe 1612
Db 6433 ----- 6433
QY 1613 AspGlyAlaAspAenThrValThrMetLeuGlySerPheSerGlyThrThrValProAla 1632
Db 6434 -----ATCCCTGTG 6442
QY 1633 LeuLeuAsnSerThrSerAenGlnLeuTyrLeuHisPheTyrSerAspIleSerValSer 1652
Db 6442 ----- 6442
QY 1653 AlaAlaGlyPheHisLeuGlnTyrLeuThrValGlyLeuSerSerCysProGluProAla 1672
Db 6443 -----CCGTGTGAGAGCCCA 6460
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QY 1831 GluTyrGlnAlaTrrpGluLeuGln----- 1838
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QY 3042 Leu-----AspLeuProSerMet---GlyTyrThrLeuIleThrPro 3054
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RESULT 3
US-09-341-461-1
; Sequence 1, Application US/09341461
; Patent No. 6586389
; GENERAL INFORMATION:
; APPLICANT: Hammond, Timothy G.
; APPLICANT: Veronnet, Pierre J.
; TITLE OF INVENTION: Cubilin Protein, DNA Sequences Encoding Cubilin
; FILE REFERENCE: D6148
; CURRENT APPLICATION NUMBER: US/09/341,461
; CURRENT FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: PCT/US99/01259
; PRIOR FILING DATE: 1999-01-21
; NUMBER OF SEQ ID NOS: 40
; SEQ ID NO 1
; LENGTH: 11272
; TYPE: DNA
; ORGANISM: rat
; FEATURE:
; OTHER INFORMATION: nucleic acid sequence of rat cubilin
US-09-341-461-1

Alignment Scores:
Pred. No.: 2,7e-94 Length: 11272
Score: 1384,00 Matches: 799
Percent Similarity: 32,10% Conservative: 431
Best Local Similarity: 20,85% Mismatches: 1224
Query Match: 8,15% Indels: 1380
DB: Gaps: 163

US-10-016-248-2 (1-3104) x US-09-341-461-1 (1-11272)
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Qy 684 GlyGlyPheIleGlnIleSerSerGlyThrIleLeuSerProGlyPheProAspPheTyr 703
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Qy 704 ProAsnAsnLeuAsnCysThrTyrPheIleGlnThrSerHisGlyLysGlyValPhePhe 723
Db 2857 CCAAGAGCTGTAAATTTGATCTTGCAATGATGATGCAACGCGCCCAACGATCCGTTTG 2916
Qy 724 ThrPheIleThrPheHisIleuGlu-----SerGlyHisAspTyrIleuLeuIle 739
Db 2917 GAATTCAGTTCCTTTTACCTGAGGTTTCATTAACAATGCACAAACGATCTCGGAATTT 2976
Qy 740 ThrGluAsnGlySerPheThrGlnProLeuArgGlnLeuThrGlySerArgLeuProAla 759
Db 2977 TATGACACTGCGCGCTCAGACTTTT---CTTGGAGATATGTTGAAATATCCATCCGCGCT 3033

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QY 760 ProIleSerIaGlYleuTrGlyAaenPheThraIaGlValaArpHeIleSerAaPhe 779
Db 3034 TCTCTTAAACAGC-----AACTTAATTCATAAAGCTGATATTGTGCTGACTCC 3084
QY 780 SerMetSerTyGIuGIyPheaenIleThrPheSerGIuTyraPheIuGIuProCySGlu 799
Db 3085 GCCCTTGCCACAGAGCTTTCCATTAATTAAGAGCAATGCAT----- 3129
QY 800 GIuProGIuValProIaTySerIleArgIySGlyIuGIuInPheGIyValGIaSerPthr 819
Db 3130 -----GCATCATCAGTA----- 3141
QY 820 LeuThrPheSerCySPheProGIyTyraArgIeGIuGIyThraIaArgIleThrCySleu 839
Db 3141 ----- 3141
QY 840 GlyGIyArGaArgIeLeuTrPseSerProIeuProArgCySValaIaGIuCySGlyAaen 859
Db 3142 -----TCTTAATAT 3150
QY 860 SerValThrGIyThrGIuGIyThrLeuLeuSerProAaenPheProValaAaTyraAaen 879
Db 3151 GACTATACAGATTAATTTGGAGATGCTCTCCCTCCGAACTTCCCAATATTAACCCAGT 3210
QY 880 AaenHIGIuCyValIeTyraSerIleGIuThrInProGIySGlyIleGIuLeuYsAla 899
Db 3211 AACTGGAGTGCATCTACAGATCACTGGGACTACACCAAGATGATTCATTC 3270
QY 900 ArgAlaPheGIuLeuSerGIu-----GIyAaPValleuYsValTy 913
Db 3271 ACAGACTTACCTTGGAGACTATTGGGTCAAGTGTGATATTGTAAGAAATCAG 3330
QY 914 AaPGLyAaenAaenSerAlaArgIeLeuGIyValPheSerHISerGIuMetMetGIy 933
Db 3331 GACGGAGGCTACAAACGTGCGCTGTGGATTACTGTGCTCA---GTTTGGCT 3387
QY 934 ValThraAaenSerThrPheSerSerLeuThraAaenPheIleThraPAlaGIuAaen 953
Db 3388 CTAACATCATCTCTCCACAGTAACAGCTGTGGTAAGTTAAGAGTGGCGGCACATC 3447
QY 954 ThSerIySGly----- 957
Db 3448 AGGCAAAAGGGTTCTCAGGTACTGGGAGGATCATCAAGGCTGTGAGGTAATCTC 3507
QY 957 ----- 957
Db 3508 ACCACCCACAGGTGTCATCATGCCCCAATACTACCCGATCCCTACTACAGCTCCGA 3567
QY 958 -----PheGIuLeuHISerPheSerPhe 965
Db 3568 TGCTACTGGCGGCTCGAAGCCAGTCAAGCCCTTTCAGAGTGAATTCGAAGCTTC 3627
QY 966 GIuLeuIleYsCySGlyAaPProGIyThrProIyPheGIyTyraYsValHISaPGLu 985
Db 3628 CACTG-----GAACACCAACCCAGCTGCTCTGTGATTAATTGGCCGTGTGAT 3678
QY 986 GlyHISaPheAlaGIySerSerVal-----Ser 994
Db 3679 GGGCCGACTACCAACTCCGACTGATAGATAAATTGTGGGATACGACACTGCTCC 3738
QY 995 PheSerCyAaPProGIyTyraSerLeuArgGIySerGIuLeuLeuCySleuSerGIy 1014
Db 3739 ATCCGTTCCATTAAGAGCTGATTTGTAATAAGTGAAGACTG-----ATGCAAGGT 3792
QY 1015 GIuArgIyThrTrp-----AaPArgProIeuProThrCySValaIaGIuCySGlyGIy 1032
Db 3793 CAGCT-AGGCGGCGCTTGATGATCAA---CTTCGCGAGAGATGAGCAATGTGATGAT 3848
QY 1033 -ThraIaArgGIyGIuValSerGIyGIuValLeuSerProGIyTyraProIaProTyGI 1052
Db 3849 AGTG-----AACAAAACCTTTGGCATCTCGAGAGCATTAATTAATCAATCCATATGA 3902

QY 1052 uHISaenLeuAenCySleIeTrPThrIleGIuValaGIuValGIyCySThrIleGIyLeuH 1072
Db 3903 TAAAGAACAACTTTGTAAGTGAATCCATCCAAACCAACCCGCAACCCGTGAATCAAC 3962
QY 1072 aPheLeuValPheAaPThrGIuGIuVal-----HISaPValleuArgIleTr 1088
Db 3963 GTTTCGGATTTGATGTCGAAGATTAATCAAGATGCTCCACAGATTAATGAGACTTA 4022
QY 1088 aPArgIyProValaGIuSerGIyValLeuLeuYsGIuLeuSerGIyProAlaLeuProIy 1108
Db 4023 TATGGACCCCAATGAGATGGA-----CGCTACTGTGAAATTAACATGCCCC 4070
QY 1108 aAaPLeuHISerThrPheAaenSerValaIuGIuInPheSerThraSPhePheThre 1128
Db 4071 ACCAGGGGCTACAAACAGCTCCCACTCCAGTACTGTTCCATACAGATGGATCATTC 4130
QY 1128 r---LySGInGIyPheAlaIleGIuInPheSerVal-----Se 1139
Db 4131 TGGGAAAAGGATTAAGATGACAGTTCATGCTGCTGCTGTGAGAGATGCTCG 4190
QY 1139 rThraIaThrSerCySaaenAaPProGIyIleProGIuAaenGIySerArgSerGIyAaPse 1159
Db 4191 AACCGAGGCTCTTCAGAGCCCTGGGTACCCCAACACTATCTCACAAACAAAGATG 4250
QY 1159 r---TrpGIuValaGIyAaPSerThraValPheGIuCyAaPProGIyTyraIaLeuGIu 1177
Db 4251 TATCTGAAAC-----ATTGCGGTGGCCCAAGGAGATGATTCAGCT 4292
QY 1178 -----GlySerAlaGIuI 1182
Db 4293 CACCATTCATGACTTTGATGTAATATCATCAAGCTCAACTGATGATCTCCCTGGAGAT 4352
QY 1182 e-----SerCySValYs----- 1186
Db 4353 CTATGAGGTCTGATTTTAACCTCCCAAGATAGCCCACTGTGTTCCCAATCACCGTC 4412
QY 1186 ----- 1186
Db 4413 AACGAACCCCATGACAGTCTCCAGCACTGGCAATGAATCAATCCGATTTAAGACGA 4472
QY 1187 -----IleGIuAaenArgPhePhe-----TrpGIuProSerProProThrCySleI 1201
Db 4473 TAGCACTTAATTAAGAAAGGTTTCAATGCTCTGTCGACAGCAAGTCCCT- 4521
QY 1201 eAlaProCySGlyGIyAaPLeuThrGIyProSerGIyValIleLeuSerProAaenTyPr 1221
Db 4522 -GAGGTTGTGTGAATTAATTCACCTTCCAGAGAGATTCATTCCTCAATTAACC 4580
QY 1221 oGIuProTyraProProGIyLyGIuCyAaPTrIyAaPValThraIaSerProAaPtyrA 1241
Db 4581 CAACAACATACAGACTAACAGAGATGCTCTGATCATTCAGATTGAGCGACATACCG 4640
QY 1241 IleAlaLeuValPheAaenIlePheAaenGIuInProGIyTyraaPheLeuHISleTy 1261
Db 4641 TGTCTCTGATATCATCACTGACTTGAACCTCAGATTCCTGCTTCAAGATTAAT 4700
QY 1261 rAaPGLyArGaPseSerLeuSerProIeuIleIySerPheTyGIy---SerGIuLeuPr 1280
Db 4701 GATGAGCTCAAGTTCACAAACGCCGTGCTCCAGTGTGTGGAAGAAGACAGCCGCC 4760
QY 1280 oGIyArgIleGIuSerSerSerAaenSerLeuPheLeuAlaPheArgSerAaPAlaSerVa 1300
Db 4761 TAACCTATCATCGCTTCAGAAAGACCTTTTGTGAGATTCGGGTCTGATCTTCGAG 4820
QY 1300 IserAaenAlaGIyPheValIleAaPtyrThrGIuAaenProArgIuSerCySPheAaPPr 1320
Db 4821 CCAGAAACAGGGCTTCGGGCTGAATTC-----AGGAAAGAGTGC----- 4860
QY 1320 oGIySerIleYsAaenGIyThraYsAlaGIySerAaPLeuYsLeuGIySerSerValTh 1340
Db 4861 -----GAGAGCCGATCATGACGAC-----TCTTCGATAC 4892
QY 1340 r-----TyTyraCySleHISleGIyGIyTyraGIuValaGIuGIyThrSer----- 1353

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Db      4893 TATCTTCTCCAGCTGTAACCTGACAACTATCTACACAGCAAGAACTGTTCTGGATAT 4952
Qy      1354 -----Thleuser----- 1356
Db      4953 TGAAGTCAGCCCTCATTCATCAATTAATCTCTCTTACTGCACTTCAACTTCAAAA 5012
Qy      1357 -----Cys-----IleuGlyProAapGlyys 1364
Db      5013 CAGCAGAGACTGTACAGGGACTTTGTAAGAAATTTG-----GATGCAACAGACTATGA 5066
Qy      1365 -----ProVal-----TrrAaAspProAapProVal 1373
Db      5067 CGACCTGTCCAGAGCCGTTACTGTGGTTCTCCCTGCCCAACCCATCATATGATTTGG 5126
Qy      1373 ----- 1373
Db      5127 CAATGCCCTTACCGTGAAGTTTGTCACTGATTCACAGCAGTTTGGAGGTTTCCGTGC 5186
Qy      1374 -----CysThrAlaProCysGlyGlyGlnThrValGlySerAapGlyVal 1389
Db      5187 CATCTATTCTGCATCGACATATCTGTGTGAAGCTTCTACACACTTGATGGCATCTT 5246
Qy      1389 IleuserProAapThrProGlnAapThrThrseryGlnIleCysleuThr---PheVal 1408
Db      5247 CAATAGCCCGACATCCAGAGACTACCAATCCAAATGAGAAATGTGTGGAACATTCG 5306
Qy      1408 1ThrValProLysAapThrValValPheGlyGlnPheAlaPhe--PheHisThrAla 1427
Db      5307 CAGCTCCCTGGCAACCGCTGCAACTGTCTCTTCTCTTCAATTTGGAGAAATCTCT 5366
Qy      1427 uAen-----AapValValGlyValHisAapGlyHisSerGlnHisSerAapLeu 1444
Db      5367 AACTGTAAACAGAGATTTTGTGAAATCCGAGAAAGAAATGCC-----AC 5411
Qy      1444 userSerIuserGlySerHisThrGlyGlySerLeuPro-----LeuAlaThr 1460
Db      5412 GGGCAGCTGATGTGAAGATCTGTGGAACTCCCTCCCTGGGAATTAATTCGTACAGTGA 5471
Qy      1460 rSerAapGlnValLeuIleLysPheSerAlaLysGlyLeuAlaProAlaArgGlyPhe 1479
Db      5472 GGCACATAGTCTATAGGTCGATTTGTCTGATGCTCAGAGCACTGGCATGGGCTTCCA 5531
Qy      1479 ----- 1479
Db      5532 GGCAGGTTCAAAAATATATTGTCATATATATATTGTGGAACTCATAGGAAATCGC 5591
Qy      1479 ----- 1479
Db      5592 ATCTCCCTTCGGCTGGAATAACCCCTACAACTCCAAATTAAGGATGTAATGT 5651
Qy      1480 -----HisPheValTyrglnAlaVal-----ProArgHis 1490
Db      5652 GAGCAGCATATCATTTATCCACGGTAGATCTTAGAGATGACATAGAACCCACAGAA 5711
Qy      1490 r----- 1491
Db      5712 CTGCTTTTANGACAGTTTAAAGATTATGATGATTGACATCAATCCCTCATTTGG 5771
Qy      1491 aThrGlnCysSerSerValProGluProArgTyrglyLysArgLeuGlySerAapPhe 1511
Db      5772 CACTTACTGT-----GTAACCAAGACAGAAATCCTTTACGTC 5807
Qy      1511 rValGlyAlaIleValArgPheGlnCysAapSerGlyTyrglnAlaLeuGlnGlySerProG 1531
Db      5808 CAGTAGAAACTATATCTGACATTCAGATTCTTCGAGCTCTGTGTGACAGAAAG----- 5862
Qy      1531 uIleGlnCysLeuProValProGlyAlaLeuAlaGlnTrp-----AapVal 1546
Db      5863 -----GATTCCTTCTGGAGTGGTTTGCAGTAGATGTTTCTGA 5900
Qy      1546 1SerAlaProThrCysValValPro-----CysGlyGlyAapLeuThr-----GluArg 1562

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QY 1877 -ValLeuThrCysGlnHnIleGlyThrAsnArgAsn-----TpaE 1889
Db 6634 CTACTTTGAATGGTGTACAGAGCCCACTGCAATGCACGTGTGTTCCAAATTGTGTGG 6693
QY 1889 pHISProLeuProIysCysGluVal----- 1897
Db 6694 CCACACTGTGCTCATAGTGGTATCTCTGAGAGAAAGAAATATACTTGAAGTTTACAC 6953
QY 1898 -----ProGlyGly 1901
Db 6954 TGACGGTGTTCCTCACTACATGAGATTCAGGCCAAGTACTTATAGCTCTCTGTGGAGG 7013
QY 1901 YAsnIleThrsSerSerAsnGlyThrValIYrSerProGlyPheProSer---ProIYrSe 1920
Db 7014 AACAGTCTCAGGGGACAGTGGAGTCATCAGAGACATTTGGCTACCCGACCTTCCGATGC 7073
QY 1920 rSerSerGlnAhpCysValItrPLeuIleThrValIProIleGlyHnIleGlyValArgLeuAs 1940
Db 7074 AAACAATGTGTTTGTGATGGTTTATCCGAGGCTCCAGAGACACTCACTCACTGTGAC 7133
QY 1940 nLeuSer-----LeuGlnHnThrgluPro-----SerGlyAspPheIleThrIleTr 1956
Db 7134 TTTTGAAGATTTTAACCCTTCAGAGCTCTCCGTGTGACAAAGACTTGTGAGATCTG 7193
QY 1956 pAspGlyProGlnHnThraIleProArg---LeuGlyValPheThrsrSerMetAlaly 1975
Db 7194 GGAA-----AACCATACCTCTGAGAGAGATTCTGGGAGATATTGTGAAATCCCACTCC 7247
QY 1975 elvSrThValGlnSerSerSerAsnGlnValLeuLeuIYrPheHnIleArgPheAlaIaln 1995
Db 7248 TAGCAGAGTTGACACTTCACAGCAATGTGCTCCGTCAAGTTGTGCACAAAT----- 7299
QY 1995 rGlyGlyIlePheHnIleAlaIlePheSerAlalyrProLeuThrIYcysrProProth 2015
Db 7300 -GGCTCTGTCACTCCCTCAGAGATTAGG----- 7326
QY 2015 rIleLeuProAsnIleGluValIValThrgluAsnGluIuPheAsnIleGlyAspIleVa 2035
Db 7326 ----- 7326
QY 2035 lArgIYrArgCysLeuProGlyPheThrLeuValGlyAsnGluIleLeuThrCysIysLe 2055
Db 7326 ----- 7326
QY 2055 uGlyThrIYrLeuGlnPheGlnGlyIuIProProIleCys-----GluValHisCysPr 2073
Db 7327 -----CTGCAAGTTTAAGTCCAGCAGACAAAGTGTGTGGGGATTATACAGGCC 7376
QY 2073 cThrAsnGluLeuLeuThrasPserThrglyValIleLeuSerGlnSerIYrProGlySe 2093
Db 7377 T-----ACTGGCACTTACTTCTCCCAACTACCCAAACCC 7412
QY 2093 rIYrProGlnPheGlnThrcysSerIYrLeuValArgValGluIProAspIYrAsnIleSe 2113
Db 7413 AAATCTCATGCCGGATCTGTAGTGTGAGACATCACTGTACAGAAAGAAAGGCGGATGCT 7472
QY 2113 rLeuThrValGluIYrPheLeuSerGluIYrGln-----TyAspGluIuPheG 2129
Db 7473 CCGAGAGTTTACCAACTGAGCGTGAAGTCCAGCCATCTTGAACAGTGAAGACACTCAT 7532
QY 2129 uIlePheAspGlyProSerGlyGlnSerProLeuLeuValAlaLeuSerGlyAsnIYrSe 2149
Db 7533 CGTATTCATGGCATTAAGAACCACTGCCCTACTACAGAAACTGTGACGCGGTGA 7592
QY 2149 rAlaIProLeuIleValIThrsSerSerAsnSerValIYrLeuArgIYrPserSerAspH 2169
Db 7593 TGTGACCAATGAATTCAAATCTTCAGAGAACACACAGTGAAGTGTATTTTCATGTATG 7652
QY 2169 sAlaIYrAsnArgIYrGlyPheIYrIleArgIYrSerAlaIProIYrCysSerLeuProAr 2189
Db 7653 CTCGGGCGGTATGAGAGGCTTC-----ACTGCTTCTTACACCTCTACTGAA 7700

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QY 2189 sAlaIProLeuHnIleGlyPheIleLeuGlyGlnThrsSerThrglnProGlyGlySerIleH 2209
Db 7701 TGCAGTGTGTGGTGAATTTCTT-----CCAACTGTCTCCGGTGAACCTT-- 7746
QY 2209 sPheGlyCysAsnAlaGlyIYrIYrArgLeuValGlyHisSerMetAlaIleCysThrArgH 2229
Db 7747 -----TCTCTCCGCTATATAT----- 7764
QY 2229 sProGlnGlyIYrHisLeuThrPserGluAlaIleProLeuCysGlnAlaLeuSerCysG 2249
Db 7765 -----GG 7766
QY 2249 YLeuProGluAlaIProIYrAsnGlyMetValPheGlyGlyIYrThrValGlyIYrThr 2269
Db 7767 AATCGGTATTTATGCCAGAAC-----CTAAGCTGTGAATGAGCTCTCAGTAATCC 7817
QY 2269 sAlaValIYrSerCysSerGlyIYr---TyHnIleGlnAlaGlyAlaGluAlaIleThrAl 2288
Db 7818 AATCGGGAATAATTCATCATAGTATCTATTTCTAGAACTTCCATTGAAGATCATCA 7877
QY 2288 aGluCysLeuAspThrglyLeu----- 2295
Db 7878 AGACTGTACATTGATATGCTCTGAGTTTCAGATGAGGAGTGTATGGCCCTGATAGA 7937
QY 2296 ---TpsSerAsnArgAsnValIProProGlnCysValIProValIThrcysrProAsp----- 2312
Db 7938 GAAGTTCTGTACCTGTGACAGCAGCAAGCGCCCTGTGTGATCCCTTACCCTCAGGTGC 7997
QY 2313 -----ValSerSerIleSerValGluHnIleGlyIYrIYrIYrIYrIYrIYrIYr 2329
Db 7998 GATAGCGCTTCGTACACAAATGAGCGGTGAAATATCTGA-----TTCATAT 8045
QY 2329 rGlnIYrGlnPheGlnAlaGlnLeuMetLeuIleCysAspProGlyIYrIYrIYrIYrIYr 2349
Db 8046 AGAGTATCTCTT-----ACAATTGTGTGATTCAGATTCAGACAG 8084
QY 2349 YGlnArgValIleArgCysGlnAlaAsn-----GlyIYrIYrSerLeuG 2364
Db 8085 TCACATGAGATGATCTCAAGTCAAGTCTTATCCAACTTGTACAGTGAAGACC----- 8139
QY 2364 YAspSerThrProThrcysArgIleIleSerCysGlyGluLeuProIleProProAsnG 2384
Db 8140 -----CACTGTTCATGGCTGTGAAGCCCGAGAG 8171
QY 2384 YHisArgIleGly---ThrLeuSerValIYrIYrAlaIlePheSerCysAsnSe 2403
Db 8172 GCACACATCACTCACTCACTCAGTACTTCTTTCGAGGCTCATCCAACTTGCACTTC 8231
QY 2403 rGlyIYrThrLeuValGlySerArgValArgGluCysMetAlaAsnGlyLeuIYrPserG 2423
Db 8232 AGACTCCGCTCACTGTC-----AGSAAATGTGACTCCCCAG 8267
QY 2423 YSerGluValArgCysLeuAlaGlyHisCysGly-----ThrProGluProIleValAs 2441
Db 8268 ATCGCCGCTC-----ATAGACAGATACTGTGGAAGTCAAGTCCCAAGCGGATACAGTGC 8321
QY 2441 nGlyHis-----IleAsnGlyGluAsn----- 2448
Db 8322 TGTTCACCAACAATTATAGTACTTTTAAACAACAATCAAGAGGCAAACTCGGATTC 8381
QY 2449 -TySerIYrArgIYrSerValIYrGlnCysAsnAlaGlyPheArgLeuIleGlyMe 2468
Db 8382 TTATTCACAATGAGACCAACAAGCTTTAGTGTGGGGAACATTCCTCAGCTAATGG 8441
QY 2468 tSerValArg----- 2471
Db 8442 TACATTCAAATCTCTCACTGGCTCAGACATTCAGAAAAACAGCAGATGCTCTGGAC 8501
QY 2472 ---IleCysGlnGlnAspHnIleSTrp-----SerGlyIYrThrProPheCysValIYr 2488
Db 8502 AGTATTCATCAAGATTAAGTAAACACTGGAGATTAGCTTTGACAGCAATTTCCGAATCC 8561
QY 2488 O----- 2488

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D 8562 CAGCAGTGAAGCAGAGTGTGAGAACAGCTTGAGAGTTGGGAGGAGCTTGATGAT 8621
Q 2489 -----IleThrCysGlyHisProGly---AsnProValAsnGlyLe 2501
D 8622 CAATAGAACCTCTTGAACAGAGAGCTGTGAGATGTGGCTCCAACTCCCAT-----GT 8675
Q 2501 uThrGlnGlyAsnGlnPheAsnLeuAsnAspValValLysPheValCysAsnProGlyTy 2521
D 8676 CACATCAGGGAGAACATTTTC-----ACTGCTGTCTT 8705
Q 2521 tMetAlaGlnGlyValAlaIArgSerGlnCysLeuAlaSerGlyGlnTrpSerAspMetLe 2541
D 8706 CCAATCGAGAGATGGA-----GCCAGGCGCTTCTGTGATCTTCAT 8750
Q 2541 uProThrCys---ArgIleIleAsnCysThrAspProGly---HisGln----- 2555
D 8751 TAGCCGGTGGCGAGACATTCAT---ACCTCCCTGTGTACATCATCTCTCCAACTT 8807
Q 2556 GlnAsnSerValArgGlnValHisAlaSerGly---ProHisArg----- 2569
D 8808 CCCGAGCATATACACAAACAAATGAATGACCTCACTCATAGACGCTGACCTCACTG 8867
Q 2570 -----PheSerPheGlyThrThrValSerTyArgCysAsn 2581
D 8868 TCTGTGATCCTGACTTTTGTCTCTTCATTTGGAAGATGCGTCAGCTATCACCGGAC 8927
Q 2582 -----HisGlyPheTyLeuLeuGlyThrProValLeuSerCysGlnGly 2596
D 8928 CTGTGATCATGATGCTGTGACATCAAAAGGTGTAACTCTTCCTCCACTCTCTGT 8987
Q 2597 AspGlyThrTrp-----AspArgProArgProGlnCysLeuLeuValSerCysGlyHis 2614
D 8988 GACCATATGTGTGTTCTGAACCTTGGCTCCCTCACTGT----- 9026
Q 2615 ProGlySerProProHisSerGlnMet-SerGlyAspSerTyThrVal-----GlyAl 2632
D 9027 ---GGAGGCGCCAGTGTGCTCAACTTCTATTCGATGACATACACACAGACTTTGGCTT 9083
Q 2632 aValValArgTySerCysIleGlyLysArgThrLeuValGlyAsnSerThrArgMetCys 2652
D 9084 CAAGATTTCCATACAGAGCCATCACTGTGTGGATCTAACATGAATCTCTGGAAATCT 9143
Q 2652 eGlyLeuAspGlyHisTrpThrGlySerLeuProHis----- 2664
D 9144 TAGGAGCCCTTCTACTCATACAGCAACTACCCCAACAACTCTACTGTGTACAGCCT 9203
Q 2664 ----- 2664
D 9204 CCATGTTAGAACAGCAGAGATGAATTAATAGTTCAATGATTTCCATGTGCTCTTC 9263
Q 2665 ---CysSerGlyThrSerValGlyValCysGlyAspProGlyIleProAlaHisGly 2682
D 9264 CAACCTTTGTGCATGACTCTCTCGAGAGTGTGATGTGCTCCAGATGGAATGATCAT 9323
Q 2682 yIle---ArgLeuGlyAspSerPheAspProGlyThrValMetArgPheSerCysGlyAl 2701
D 9324 TCTTGAAAGTCTGTGTGTCTCAGCGCTCAAACTGTTAAGACCAATAGCAGCCT 9383
Q 2701 aGlnHisValLeuArgGlySerGlyArgGlyThrCysGlnAlaAsnGlySerTrpSer-- 2720
D 9384 GACCTGTGTTCACAGACAGATTTCTTCACAAACAGCAAG-----GGTTGGAAT 9434
Q 2721 -----GlySerGlnProGlnCysGlyValIle----- 2729
D 9435 ATTTTCCGAGAGCAATAGGGCCACAGAGAGATGTGTGATACCTGACCGAGAGCAA 9494
Q 2730 ---SerCysGlyAsnProGlyThrProSerAsnAlaArgVal----- 2742
D 9495 CCAGAGCTTTGTGTCTCTGATTCGATTCGAATGAGCGCTATGACAAAGGCTTCAGCTG 9554
Q 2743 -----ValPheSe 2745

D 9555 CATATGATACATAGTTGACACCTGAAAACAAACCTGTTAAGCTCACTTCATGTGTTCAC 9614
Q 2745 r---AspGlyLeuValPheSerSerIleValTyrgLysCysArgGlyGlyTyThrAl 2764
D 9615 TCTGAGAGGACCATTCGTCACTGGAGCTCGCTGTATGATTAATGTGAG----- 9663
Q 2764 aThrGlyLeuLeuSerArgHisCysSerValAsn-----GlyThrTrpThrGly 2780
D 9664 -----ATACAGATGGCCCAAGCATAATCTCATTTAAGTGGAAAAATTCGTGTG 9713
Q 2780 ySerAspProGlnCysLeuValIle----- 2788
D 9714 CTCCCGTAT-GCCTGCCCCATTTATCTTCCGGCTACTTCTTACGTTTCAGTTGTCT 9772
Q 2789 ---AsnCysGlyAspProGlyIleProAlaAsnGlyLeuArgLeuGlyAsnAspPh 2806
D 9773 CTGACGTAACTGTGAATAGAGGATTTAATGCAATATACCTTTGTGAGACATGCTT 9832
Q 2806 eArgTyAsn-----LysThrValThrTyrgLysCysValProGlyTyrmMetMetGly 2823
D 9833 GCGGGGGAACATATACGCAACCTCGACACTTCAMAAATGCGTATCATCACTTATTCAC 9892
Q 2823 uSerHisArgValSerValLeu-SerCysThr----- 2833
D 9893 A---CATCGGACGGCATACTCCACTGTACTTGGCTATGCGAGCTCCCCACAGAGC 9949
Q 2834 ---LysAspArgThrTrpAsnGlyThrTybProVal-----CysValAlaLeuMetC 2850
D 9950 AGGTTCAATACCTGTGTGGACTTACAGCTGCCCTCAAGACTGTCTCAAAAGTACT 10009
Q 2850 yLysPProProProLeuIleProAsnGlyLysValValGlySerAspPheMetTrpGly 2870
D 10010 TAGAATCTCAGATTCAGTACAGACTGT-----GGA 10042
Q 2870 eSerValThrTyraLysCysLeuGlnGlyTyrgLysLeuSerLeuProAlaValPheThrC 2890
D 10043 ACCGGGTGACTAGTGTGCGGTGCGAAATAT---ACAACCTTGCAGTGTTCATCC- 10098
Q 2890 yGlnGlyAsnGlySerTrpThrGlyGlnLeuProGlnCysPheProValPheCysGly 2910
D 10099 -----TCAAATGAGCACTGGCGTTGCTGTTTC-----A 10126
Q 2910 ePProGlyValProSerArgGlyArgArgGlyAspArgGlyPheSerTyArgSerServ 2930
D 10127 AGTCTGAGATTATTAACAGAACTCGCAAGTCAA-----TCTCTTATCAAGATTGCA- 10179
Q 2930 aSerPheSerCysHisPProProLeuValLeuValGlySerProArgArgPheCysGlns 2950
D 10180 -----GATTCGAAC-----AGAGATACAAACCAA 10204
Q 2950 eAspGlyThrTrpSerGlyThrGlnProSerCysIleAspProThrLeuThrThrcysA 2970
D 10205 CGTTTGGC-----AATTCGA 10219
Q 2970 laAspProGlyValProGlnPheGlyYIleGlnAsnAsnSerGlnGlyTyrgValGlys 2990
D 10220 AGACTCTGTGGTGGCTCAG---AACTATACAAATAC-----CTGACT 10261
Q 2990 eThrValLeuPheArgCysGlnLysGly-----TyrlLeuLeug 3003
D 10262 GCACCATCATTCACAGAGCCCGCAGAACACAGCATTCCTCCCTTTTATATGCTTTC 10321
Q 3003 lngLysThrThrArgGlyThrCysLeuProAsn-LeuThrTrpSerGlyThrProProAsp 3022
D 10322 AGCTGGAAGATTCACAGCAATGATG---AATGATTTCTTGAGGTAAAGAAAGCGCGCA 10378
Q 3023 CysValProHisHisCysArgGlnProGlyThr-----ProThrHisAlaAsn 3038
D 10379 GCAGACCTTACCACTGCTTGAACAATCTGTAGCAACTGTGCCCCACCGGTCTTCT 10438
Q 3039 ValGlyAlaLeuAspLeu-----ProSerMetGly 3048
D 10439 CTCAGACCAACAACTGTATCTGCACTTTCACAGCGACCACTGACTACCAACAAATGGCT 10498

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OY      3049 TyrThrLeuIleThrPro 3054
Db      10499 ATGAATTATTGGACCT 10516

RESULT 4
US-09-023-655-1265
; Sequence 1265, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1265:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6951 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g30185
; US-09-023-655-1265

Alignment Scores:
Pred. No.:
Score: 1.19e-93 Length: 6951
Percent Similarity: 1371.00 Matches: 538
Best Local Similarity: 32.87% Conservative: 266
Query Match: 22.00% Mismatches: 832
DB: 8.07% Indels: 810
Gaps: 109

US-10-016-248-2 (1-3104) x US-09-023-655-1265 (1-6951)

OY      798 CyeGluIuPProGluValProAla-----TyrSerIleArgIysGlyLeuGlnPhe 814
Db      337 TGTCGTATCTCTCCAGATCTCTGTGAATGCGATGTCATGTCATCAAGGATCCAGTTC 396
OY      815 G1yValG1yAephThrLeuThrPheSerCysPheProG1yTYrArgLeuG1uG1yThrAla 834
Db      397 -----GGATCCCAAAATTAATATTCTTGTACTAAAGGATACCACTATGTTCTCTCG 450
OY      835 ArgIleThrCys---LeuG1yG1yATgATgATgLeuTTPSerSerProLeuProArgCys 853

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Db 1063 -----TGAGCCCTGAGACCCCAATGTAAGTAATCTGTGATGATCATGGGC 1116
Qy 1211 Pro-----SerGlyValIleLeuSerProAsnTyrProGluProTyrProProGlyLys 1228
Db 1117 CAACCTTCTTAATGAGCCGCTGCTATTTCCTCA----- 1146
Qy 1229 GlucyAspTrpLysValThrValSerProAspTyrValIleAlaLeuValPheAsnIle 1248
Db 1146 ----- 1146
Qy 1249 PheAsnLeuGluProGlyTyrAspPheLeuHisIleTyrAspGlyArgAspSerLeuSer 1268
Db 1147 GTAAATCTCCACGCTTGAGCAAAAGTGAGATTGTGTGAT----- 1188
Qy 1269 ProLeuIleGlySerPheTyrGlySerGlnLeuProGlyArgIleGluSerSerSerAsn 1288
Db 1189 -----GAGGATTTCAATTAAGAGC-----AGCTTCGTCTAGT 1221
Qy 1289 SerLeuPheLeuAla-----PheArgSerAspAlaSerValSerAsnAla 1303
Db 1222 TACTGTGTCTTGCTGGAAATGAAAGCCTTTGAAATGACAGTCTCCAGTGTGAAACA 1281
Qy 1304 GlyPheValIleAspTyrThrGluAsnProArgGluSerCysPheAspProGlySerIle 1323
Db 1282 ATCTTT-----TGTCAAGTCTCCAGTTATT 1308
Qy 1324 LysAsnGlyThrArgValGlySerAspLeuLysLeu-----GlySerSerValThr 1340
Db 1309 CCTAATGGAGACACACAGGAAACCTCTGAAAGTCTTCCCTTTGGAAAGCAGTAAT 1368
Qy 1341 TyrTyrCysHis-----GlyGlyTyrGluValIleGluIleThrSerThr 1354
Db 1369 TACACATGCGACCCCAACGACAGAGGAGCGAGCTTCGACCTTCATTTGGAGAGACACC 1428
Qy 1355 LeuSerCysAlaLeuGluProAspGlyLysProValIleTrpAsnAsnProArgProValCys 1374
Db 1429 ATCGGCTGCACAGAGACCTCAAGGGAGATGGGGTTGGAGACACCCCTCGGCTGT 1488
Qy 1375 ThrAlaProCysGlyGlyGlnTyrValGlySerAspGlyValIleLeuSerProAsnTyr 1394
Db 1489 -----GGAATTCG----- 1497
Qy 1395 ProGlnAsnTyrThrSerGlyGlnIleCysLeuTyrPheValThrValProLysAspTyr 1414
Db 1497 ----- 1497
Qy 1415 ValValPheGlyGlnPheAlaPhePheHisThrAlaLeuAsnAspValIleGluValHis 1434
Db 1497 ----- 1497
Qy 1435 AspGlyHisSerGln-----HisSerArgLeuLeuSerSerLeuSerGlySerHisThr 1452
Db 1498 -----GGTCACTGTCAAGCCCAAGATCAATTTCTGTGGCAAGTGAACCAACCAACCAAT 1554
Qy 1453 GlyLeuSerLeuProLeuAlaThrSerAsnGlnValLeuIleLysPheSerAlaLysGly 1472
Db 1555 GCATCTGACTTCCCATTTGGGACATCT-----TTAAAGTTCGAAATGCCGGCTCT 1602
Qy 1473 LeuAlaProAlaArgGlyPhe-----HisPheValTyrGlnAlaVal 1486
Db 1603 GAGTACACGAGGAGGACATTTCTATCATCATGCTAGATACCGTGTGTGTAAGT--- 1659
Qy 1487 ProArg-----ThrSerAlaThrGlnCysSerSerValProGluProArgTyrGlyLys 1504
Db 1660 CCCAAAGATGTCTTAAACGTAAATCATGTAAACTCTCCAGATCCAGTAAAGGAGATG 1719
Qy 1505 ---ArgLeuGlySerAspPheSerValGlyAlaIleValArgPheGluCysAsnSerGly 1523
Db 1720 GTGATGTGATCAGACATCCAGGTGTGATCCAGATCAACTATTTCTTGACTACAGGG 1779
Qy 1524 TyrAlaLeuGlnGlySerProGluIleGluCysLeuProValProGlyAlaLeuAlaGln 1543
Db 1780 CACGAGCTCATGTGTCACTATCTGTGAATGTATC---CTCTGGGGGAATGTGCGCAT 1836

Qy 1544 TrpAsnValSerAlaProThrCysVal-----ValProCysGlyGlyAsnLeuThrGluArg 1562
Db 1837 TGGAGCAGAGCCGCCAATTTGTCAACGAAATTCCTGTGGCTACCCCAATGCGCC 1896
Qy 1563 ArgGlyThrIleLeuSerProGlyPheProGluProTyrLeuAsnSerLeuAsnCysVal 1582
Db 1897 AATGAGATTTCTATTAGCACCAACAGAGAAATTTCCATATGGATCA----- 1944
Qy 1583 TrpLysIleValValProGluGlyAlaGlyIleGlnIleGlnValIleSerPheValThr 1602
Db 1945 -----GTGTGACCTACCGCTGC 1962
Qy 1603 GluGlnAsnTrpAspSerLeuGluValPheAspGlyAlaAspAsnThrValThrMetLeu 1622
Db 1963 AATCTCGAAGCCGAGGAGAGAAAGTGTAG-----CTGTGC 2001
Qy 1623 GlySerPheSerGlyThrThrValProAlaLeuLeuAsnSerThrSerAsnGlnLeuTyr 1642
Db 2002 GTTGAGCCCTC-----ATATACGACACCGACATGAC----- 2034
Qy 1643 LeuHisPheTyrSerAspIleSerValSerAlaAlaGlyPheHisLeuGluTyrLysThr 1662
Db 2035 -----GATCAA 2040
Qy 1663 ValGlyLeuSerSerCysProGluPro-----AlaValProSer----- 1675
Db 2041 GTGGGATCTGGAGCGCGCCGCCCTCAGTGCATTTACTTAACAATCAGCGCTCCA 2100
Qy 1676 -----AsnGlyValLysThrGlyGluArg-----TyrLeuValAsnAspVal 1689
Db 2101 AATGTGAAATATGAAATATGTATCTGACACAGAACTTATTTCTTAATGAAGTT 2160
Qy 1690 ValSerPheGlnCysGluProGlyTyrAlaLeuGlnGlyHisAlaHisIleSerCysMet 1709
Db 2161 GTGAGATTGTAGTGTGACGCTGCTGTGATGAAGAGACCCCGCTGGAAGTGCAG 2220
Qy 1710 ProGlyThrValArgAspTrpAsnTyrProProProLeuSerValIleGlnCysGlyGly 1729
Db 2221 -----GCCCTGAACAATAGAGAGCGGAGCTCAAGCTGCTCCAGGATATG--- 2268
Qy 1730 ThrValGluGluMetGluGlyValIleLeuSerProGlyPheProGlyAsnTyrProSer 1749
Db 2268 ----- 2268
Qy 1750 AsnMetAspCysSerTrpLysIleAlaLeuProValGlyPheGlyAlaHisIleGlnPhe 1769
Db 2268 ----- 2268
Qy 1770 LeuAsnPheSerThrGluProAsnHisAspTyrIleGluIleArgAsnGlyProTyrGlu 1789
Db 2269 -----CAGCCACCTCCAGATGCTCTG----- 2289
Qy 1790 ThrSerArgMetMetGlyArgPheSerGlySerGluLeuProSerSerLeuLeuSerThr 1809
Db 2289 ----- 2289
Qy 1810 SerHisGluThrThrValTyrPheHisSerAspHisSerGlnAsnArgProGlyPheLys 1829
Db 2290 -----CATGCTGAGGATCCCAAG----- 2310
Qy 1830 LeuGluTyrGlnAlaTyrGluLeuGlnGluCysProAspProGluProPheAlaAsnGly 1849
Db 2311 -----GACAGAGACAATCTT----- 2325
Qy 1850 IleValArgGlyAlaGlyTyrAsnValGlyGlnSerValThrPheGluCysLeuProGly 1869
Db 2326 -----TACCCGGGACAGAAAGTGTCTACAGCTGTGACCCGGC 2364
Qy 1870 TyrGlnLeuThrGlyHisProValLeuThrCysGlnHisGlyThrAsnArgAsnTrpAsp 1889
Db 2365 TATGACCTCAGAGGGGCTGCTGTATGCTGCACA-----CCCAAGAGAGACTGAGC 2418

Db	4234	CCATTGGCAGGCTCAGATCCCAATTATATGCTTT-----GAGTTTCCAGTC	4281
Oy	2510	AenbapvalvalyephevalcyebapProgllyrthymetlaagluylalalargser	2529
Db	4282	GGGACCTCTTGAATTAATTAATGCGCTCGCTGGGTATTTTGGGAAAMTTCTTATCTCC	4341
Oy	2530	GlnCybLeuAlaSerGlyGlnTrpSerArmelleuProthrCyargXlAlaAsnCyb	2549
Db	4342	---TGCCTAGAAATTTGGTCTGGCGAAGTGTGAAGACAACTGAGCGAAATTCAGT	4398
Oy	2550	ThraerpProgllyhlaeglnGluabnservalarglnvalhlaalaserGlyProhlaarg	2569
Db	4399	GGACCTCCACAGAACCTTCATAGAGATGGCGATATAAACACAGAT-----	4446
Oy	2570	PheserphegllythrThvalserTyargCyabnsihlgllyPheTyLeuLeuglyThr	2589
Db	4447	ACACAGTTTGGATCAACAGTTAATATCTTGTATGAAGGTTTCCAGCTCATGGTCC	4506
Oy	2590	ProvalleuserCyebGlnGlyAargply-----ThrTrpAargProargProbin	2606
Db	4507	CCATCTACTACTGTCTGCTGCCTCAGGCAATAATGTCAATGGAGATAAGAGCACATATT	4566
Oy	2607	CysLeuLeuAlaSerCyebGlyhlaerProgllyserProhlaSerGlnmetSerGlyAar	2626
Db	4567	TGTGAGATCATATCTTGT-----GAGCCACCTCCACACATATCCAAATGGAGAC	4614
Oy	2627	SerTythr-----ValglalavalalargTyserCyb--	2638
Db	4615	TTCTTACAGCAACAATAGAAACATCTTTTCAAAATGGAACGGTGGTAACTTACAGAGTCCAC	4674
Oy	2639	-----llegllybargThrLeuValGlyabn	2647
Db	4675	ACTGGACCAATGGAGAACAGCTGTTTGTAGCTTGGGAGAACGGTCAATATAT-----	4728
Oy	2648	SerThraTgmetCyebGlyLeuabrglyhlaerTrpThrglyserLeuProhlaCyserGly	2667
Db	4729	TGCACACAGCAAGATGATCAAGTGTGTGGAGACAGCCCTCCGCTGATTTTCT	4788
Oy	2668	ThiservalGlyvalCyebGlyAarProgllyleProalanhlaeglyleargLeuGlyAar	2687
Db	4789	ACTAAT-----AAATGCACAGCTCCAGAGTT--GAAMATGCATTAAGATACACAGA	4839
Oy	2688	Ser-----PheAarProgllyThrvalmetAargPheSerCyebGluAlaGlyhlaVal	2704
Db	4840	AACAGAGATTTCTTTCCCTCAGTGAATCATCAATTTAATGATGCACCCGGGTGTCTC	4899
Oy	2705	LeuAargGlyserSerGluargThrcCyebGlnAlaanglyserTrpserGlySerGlnPro	2724
Db	4900	ATGTGAGGCTCCACACTGTGCAGTCCAGACCAATGGCAAGTGGGGGCCCAAGCTGCCA	4959
Oy	2725	GluCyebGlyvalhlaSerCyebGlyAarProgllyThrProSerAamAlaargValAalphe	2744
Db	4960	CACGTCTCCAGGGTGT---TGTCAGCGGCTCCAGAAATCTGCAGATGAGACATACCTTA	5016
Oy	2745	Ser-----AargGlyLeuvalAalPheSerSerSerlevalTyrgluCyabargGluGlyTy	2762
Db	5017	AGCCATCAGAGCAACTTTTCACTTGGGAGAGAGTGTCTACAGCTGTGAGCCCAAGCTAT	5076
Oy	2763	TyrAlaThrGlyLeuLeuSerAarghlaCybSerValanglyThrTrpThrGlySerAar	2782
Db	5077	GACCTCAGAGGGGTGCGTCTGTGACATGCACGCCCCAGGAGACTGGAGCCCTGAAGCC	5136
Oy	2783	ProGluCybLeuValAlaAsnCyebGlyAar-----ProGlyleleProAlaAsnGlyLeu	2800
Db	5137	CCTAATATGACAGTGAATAATCTCTGTATGACTTCCCTGGGCAACTCCCTCATAGCCGTGTG	5166
Oy	2801	ArgLeuGlyAamAarPheargTyraenlyThrValThrTyrglnCybValProgllyTy	2820
Db	5197	CTACTTCACTTAATCTCCAGCTTGGGCAAAAGGTGCTCTTGTGTGGATGAAGAGGTTC	5256
Oy	2821	MetmetGluSerhlaArgValSer-----ValleuserCybThrlyAarArgThrTrp	2838
Db	5257	CGATTAAAGCGAGGTCTGTAGTCAATGTGTCTTGGTGGAATGAATGA--GCCCTTTGG	5313

QY	2839	AsnGlyThrLysProValCysGlyAlaLeuMetCysLysProCysProLeuIleProAsn	2858
Db	5314	AATGACGCTGCTCCAGTGTGTGAAACAATCTTTGTGTCCAATCTCCAGCTATCTTAT	5373
QY	2859	GlyLysValValGlySer-----AspPheMetTrpGlySerSerValThrTyrAla	2875
Db	5374	GGAGAGACACAGAGAACTCCTTTGGAGATATTCCTCATGGAAAAAATATCTTACGCA	5433
QY	2876	Cys-----LeuGluGlyTyrGlnLeuSerLeu	2884
Db	5434	TGCCACACCCACCCGACAGAGGATGACCTTCAACCTCATTTGGG---GAGAGCTTCATC	5490
QY	2885	ProAlaValPheThrCysGluGlyAsnGlySerTrpThrGlyIleuLeuProGlnCys--	2903
Db	5491	CGCTGCACAGATGACCTCTCAAGGAAATGGGGTTGGAGCAGCCCTGCCCTCGCTGTGA	5550
QY	2904	-----PheProValPheCysGlyAspProGlyValProSerArgGlyArgGluAsp	2921
Db	5551	CTTCTGTGTCCTGCTGCTGCTGCCCATTCACCCAAAGATCCAAAAGGGCATTTACTTGGA	5610
QY	2922	ArgGlyPheSerTyr-----ArgSerSerValSerPheSerCysHisProProLeu	2938
Db	5611	GGACACGATCTCTATATCTTCTCGGAGTGCACATCAGCTACACTTGTGACCCCGGCTAC	5670
QY	2939	ValLeuValGlySerProArgArgPheCysGlnSerAspGlyThrTrpSerGlyThrGln	2958
Db	5671	CTGTATTGAGGAAAAAGGCTTCATTTTCTGTACAGACAGGAAATCGAGCCAAATTGGAT	5730
QY	2959	ProSerCysIleAspProThrLeuThrThrCysAlaAspProGlyValProGlnPheGly	2978
Db	5731	CATTATTGCAGAAAGAA-----GTAATATGTAGCTTCCA---CTGTTATGAAATGA	5778
QY	2979	IleGlnAsnAsn-----SerGlnGlyTyrGlnValGlySerThrValLeuPheArg	2995
Db	5779	ATCTCGAAGAGTTAGAAATGAAAAAGTATATCATATGAGATTTATGTGACTTTGAAG	5838
QY	2996	CysGlnLysGlyTyrLeuLeuGlnGlySerThrThrArgThrCysLeuProAsnLeuThr	3015
Db	5839	TGTGAAGTGGGTATCTACTCTGGAAGCAGCTCCCTGCAGCCAGTCCAGCGCGATGACAGA	5898
QY	3016	TrpSerGlyThrProPro 3021	
Db	5899	TGGGAC-----CCTCCT 5910	

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: PRIOR FILING DATE: 2000-04-25
: PRIOR APPLICATION NUMBER: 09/488,725
: PRIOR FILING DATE: 2000-01-21
: NUMBER OF SEQ ID NOS: 1105
: SOFTWARE: pc FL_genes Version 1.0
: SEQ ID NO 255
: LENGTH: 7313
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (13)..(6147)
: US-09-620-312D-255

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Alignment Scores:	
Pred. No.:	1,3e-93
Score:	1771.00
Percent Similarity:	37.87%
Best Local Similarity:	22.00%
Query Match:	8.07%
DB:	4
Length:	7313
Matches:	538
Conservative:	266
Mismatches:	832
Indels:	810
Gaps:	109

US-10-016-248-2 (1-3104) X US-09-620-312D-259 (1-7313)

OY		798	CySGluGluProGluValProAla-----TyrSerIleArgGlyLeuGlnPhe	814
OY		337	TGTCGTAATCCCTCCAGATCCTGTGAAATGGCAGTGTGCATGTATCAAAAGCATCCAGTTC	396
OY		815	GlyValGlyAspThrLeuThrPheSerCysPheProGlyTyrArgLeuGluGlyThrAla	834
OY		397	-----GGATCCCAATTGAATTAATCTTTTACTTAAAGGATACCGCATCTTGGTTCCTGG	450
OY		835	ArgIleThrCys---LeuGlyGlyArgGArgLeuTyrPheSerProLeuProAlaCys	853
Db		451	TCTGCCACATGATCATCTCAGGTGTACTGTGCATTTGGAGATTAATGAACACCTATTGTT	510
OY		854	---ValAlaGluCysGlyAsnSerValThrGlyThrGlnGlyThrLeuLeuSerProAsn	872
Db		511	GACAGAAATTCCTGTGGGCTACCCCCCACCACATCACCAGTAAGATTTGCATTGACACCAAC	570
OY		873	PheProValAsnTyrAsnAsnAsnIleGluCysIleTyrSerIleGlnThrGlnProGly	892
Db		571	-----AGAGAGAAATTTTCACTATGAGTACAGTGCATGCTACCGCTGCATCTGGAG	621
OY		893	LysGlyIleGlnLeuIleuYalAlaArgAlaPheGluLeuSerGluGlyAspValIleuYal	912
Db		622	AGCGGAG-----GGGAGAAAGAGGTTTGAGCTT---GTGGGTAGAGCC---TCCATA	666
OY		913	TyrArgGlyAsnAsnAsnSerAlaArgLeuLeuGlyValPheSerHisSerGluMetMet	932
Db		667	TACTGCACCACGAAATGACGATCA-----GTGGGATCTGGAGCGGCCGCCCTCAG	720
OY		933	GlyValThrLeuAsnSerThrSerSerSerLeuTrpLeuAspPheIleThrAspAlaGlu	952
Db		721	TGCATTATAACCTAAC-----	735
OY		953	AsnThrSerLysGlyPheGluLeuHisPheSerSerPheGluLeuIleLysCysGluAsp	972
Db		736	-----AAATGACGGCT	747
OY		973	ProGlyThrProLysPheGlyTyrLysValHisAspGluGlyHisPhe-----AlaGly	990
Db		748	CCAAATGTGGAATAAT---GGAATATTGGATGTGACAAACAGAAAGTTATTTTCTTAAT	804
OY		991	SerSerValSerPheSerCysAspProGlyTyrSerLeuAspGlyLysSerGluLeuLeu	1010
Db		805	GAACTGTGGAGTTTAAGGTGTCAAGCTGAGCTTTGTCAAGAAAGGACCCCGCGTGTGAAG	864
OY		1011	CysLeuSerGlyGluArgGlyThrTrpAspArgProLysProCysValAlaGluCys	1030
Db		865	TGCCAGGCGCTGAAACAA-----TGGAGCCGAGAGCTTACCAAGCTGCTCCAGGGTATGT	918
OY		1031	GlyGlyThrValArgGlyGlyValSerGlyGlnValLeuSerProGlyTyrTrpAlaPro	1050

[illegible]

Db 1489 -----GGAAATTCG----- 1497
 Qy 1395 ProGlnAenYrThrSerGlyGlnIleCysLeuYrPheValThrValProIyAsnYrProSer 1414
 Db 1497 ----- 1497
 Qy 1415 ValValPheGlyGlnPheAlaPhePheHleThrAlaLeuAsnProValIleGluValHis 1434
 Db 1497 ----- 1497
 Qy 1435 AsnGlyHisSerGln-----HisSerArgLeuLeuSerSerLeuSerGlySerHisThr 1452
 Db 1498 ---GGTCACTGTCAAGCCCGCCAGATCATTTTCTGTTCCTCAAGTTGAAACCCCAACCAAT 1554
 Qy 1453 GlyLeuSerLeuProLeuAlaThrSerAsnGlnValLeuIleYrPheSerAlaIleGly 1472
 Db 1555 GCATGTGACTTTCCCATTTGGGACATCT-----TTAAAGTCAGAAATGCCGCTCT 1602
 Qy 1473 LeuAlaProAlaArgGlyPhe-----HisPheValTyrGlnAlaVal 1486
 Db 1603 GAGTACTACGGAGAGCCCATTTCTATCATCATGTCTAGATAACCTGGTCTGTCAAGT--- 1659
 Qy 1487 ProArg-----ThrSerAlaThrGlnCysSerSerValProGluProArgTyrGlyLys 1504
 Db 1660 CCCAAAGATGTCTGTAAACGTAAATCATGTAAACTCTCTCCAGATCCAGTGAATGGCATG 1719
 Qy 1505 ---ArgLeuGlySerAsnProPheSerValGlyAlaIleValArgPheGluCysAsnSerGly 1523
 Db 1720 GTGCATGTGATCAGACATCCAGGTTGGATCCAGAAATCAACTTCTTGTACTACAGGG 1779
 Qy 1524 TyrAlaLeuGlnGlySerProGluIleGluCysLeuProValProGlyAlaLeuAlGln 1543
 Db 1780 CACCGACTCATGTGTACTACTATCTGCTGAATGATC---CTCTGGGCAATGCTGCCCAT 1836
 Qy 1544 TrpAsnValSerAlaProThrCysVal---ValProCysGlyGlyAsnLeuThrGluArg 1562
 Db 1837 TGGAGCAGAAAGCCGCAATTTGTCAAGAAATTCCTTGTGGGCTAACCCCCACCATGGCC 1896
 Qy 1563 ArgGlyThrIleLeuSerProGlyPheProGluProTyrLeuAsnSerLeuAsnCysVal 1582
 Db 1897 AATGGAATTTTCATTGACACCCACAGAGAAATTTTCAATGTGATCA----- 1944
 Qy 1583 TrpIleValValProGluGlyAlaGlyIleGlnIleGlnValValSerPheValThr 1602
 Db 1945 -----GTGGTACCTTACCGCTGC 1962
 Qy 1603 GlnGlnAsnTrpAsnSerLeuGluValPheAsnGlyAlaAsnAsnThrValThrMetLeu 1622
 Db 1963 AATCCCGAAGCGGAGGAGAAAGCTTTTGAG-----CTTGTG 2001
 Qy 1623 GlySerPheSerGlyThrThrValProAlaLeuLeuAsnSerThrSerAsnGlnLeuTyr 1642
 Db 2002 GGTAAGCCCTCC-----ATATACGTGCACCAACCAATGAC----- 2034
 Qy 1643 LeuHisPheTyrSerAsnIleSerValSerAlaIleGlyPheHisLeuGluTyrLeuThr 1662
 Db 2035 -----GATCAA 2040
 Qy 1663 ValGlyLeuSerSerCysProGluPro-----AlaValProSer----- 1675
 Db 2041 GTGGGCAATCTGAGCGGCGCGGCGCTCAGTGCATTTACTTAAACAATGACGCGCTCA 2100
 Qy 1676 -----AsnGlyValIleThrGlyGluArg-----TyrLeuValAsnAspVal 1689
 Db 2101 AATGTGAAAATGGAATATGTGTAATGACAAACAGAACTTATTTCTTAAATGAAGTT 2160
 Qy 1690 ValSerPheGlnCysGluProGlyTyrAlaLeuGlnGlyHisAlaHisIleSerCysMet 1709
 Db 2161 GTGAGTTTAAAGTTCAGCTCGCTTGTGTCTATGAAAGAACCCCGCTGTGAAGTGCAG 2220
 Qy 1710 ProGlyThrValArgArgTrpAsnYrProProProLeuGlyAlaGlnCysGlyGly 1729
 Db 2221 -----GCCCTGAACAATGGAGCGGAGCTACCAAGCTGCTCCAGAGTATGT----- 2268

Qy 1730 ThrValGluGluMetGluGlyValIleLeuSerProGlyPheProGlyAsnYrProSer 1749
 Db 2268 ----- 2268
 Qy 1750 AsnMetAsnProSerTrpIleValLeuProValGlyPheGlyAlaHisIleGlnPhe 1769
 Db 2268 ----- 2268
 Qy 1770 LeuAsnPheSerThrGluProAsnHisAspTyrIleGluIleArgAsnGlyProTyrGlu 1789
 Db 2269 -----CAGCCACCTCCAGATGCTCTG----- 2289
 Qy 1790 ThrSerArgMetMetGlyArgPheSerGlySerGluLeuProSerSerLeuLeuSerThr 1809
 Db 2289 ----- 2289
 Qy 1810 SerHisGluThrThrValTyrPheHisSerAsnHisSerGlnAsnArgProGlyPheLys 1829
 Db 2290 -----CATGCTGAGCGTACCCAAAG----- 2310
 Qy 1830 LeuGluTyrGlnAlaTyrGluLeuGlnCysProAsnProGluProPheAlaAsnGly 1849
 Db 2311 -----GACAAAGCAACTT----- 2325
 Qy 1850 IleValArgGlyAlaGlyTyrAsnValGlyGlnSerValThrPheGluCysLeuProGly 1869
 Db 2326 -----TCAACCGGCGAGAAATGTTTCTACACCTGTGAGCCGCGC 2364
 Qy 1870 TyrGlnLeuThrGlyHisProValLeuThrCysGlnHisGlyThrAsnAlaAsnTrpAsn 1889
 Db 2365 TATGACTCTCAGAGCGCGCTGTATGCGCTGCACA-----CCCAAGGAGACTGAGC 2418
 Qy 1890 HisProLeuProIyCysGlyValProCysGlyGlyAsnIleThrSerSer-----Asn 1907
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 Qy 2008 LeuThrLys-----CysProProProThrIleLeuProAsnAlaGluValIleThr 2024
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 RESULT 6
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 APPLICANT: FEARON, DOUGLAS T.; KLICKSTEIN, LLOYD B.; KONG,
 MINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; IP, STEPHEN
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 TITLE OF INVENTION: COMPOSITIONS OF SOLUBLE COMPLEMENT
 RECEPTOR 1 (CR1) AND A THROMBOCYTIC AGENT, AND THE METHODS OF
 USE THEREOF
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 LENGTH: 6951
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 Score: 1362.00 Matches: 537
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 Query Match: 8.02% Indels: 810
 DB: 6 Gaps: 109
 US-10-016-248-2 (1-3104) x 5256642-1 (1-6951)
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 Qy 1229 GluCysAspTyrPheValThrValSerProAspTyrValIleAlaLeuValPheAsnIle 1248
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 Db 4342 ---TGCTTAAAAAATCTGTCTGTCTGATCAAGTGTGAAGACAACATGTGACGAATAATCATG 4398
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 Qy 2627 SerTyrThr-----ValGlyAlaValAlaArgTyrSerCys--- 2638
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 Db 4675 ACTGACCAAGATGGAAGAACGCTTTGAGCTTTGGAGAAACGGTCAATAT 4728
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 Db 4729 TGCACAGCAAGAAAGATATCAAGTTGGTGTGGAGACAGCCCTCCCTCGGTATATTCT 4788
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 Db 5077 GACCTCAAGGGGGTGGCTGTCTGTGCACTGCAGCCCAAGGGAGACTGGAGCCCTGAAGCC 5136
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 Db 5137 CTTAGATGACAGTAAATCTGTATGATCTTCTGGGCAACCTCTCATGCGCGTGG 5196
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 Qy 3016 TrpSerGlyThrProPro 3021
 Db 5899 TGGGAC-----CCTCCT 5910

RESULT 7

5472939-1
 Patent No. 5472939
 APPLICANT: FEARON, DOUGLAS T.; KLICKSTEIN, LLOYD B.; WONG,
 MINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; IP, STEPHEN
 H.; MAKRIDES, SAVVAS; MARSH, HENRY C. JR.
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US-10-016-248-2 (1-3104) x 5472939-1 (1-6951)

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 Db 942 ----- 942
 Qy 1131 GlyPheAlaIleGlnPheSerValSerThrAlaThrSerCysAsnAspProGlyIlePro 1150
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 Db 1117 CAACCTTTATAGCCGCTGTGCTATTTC--- 1146
 Qy 1229 GluCysAspTrpLysValThrValSerProAspTyrValIleAlaLeuValPheAsnIle 1248
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 DB 1309 CCTAATGGAGACACACAGGAAAACCTTGGAAGTCTTCCCTTTGAAAAAGCAGTAAT 1368
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 DB 1497 ----- 1497
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 DB 1497 ----- 1497
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 DB ----- 1602
 DB 1603 GAGTACTACGGAGGCGCATTTCTATCATGCTAGTACATCACTGCTGGTCAAGT--- 1659
 QY 1487 ProArg-----ThiSerAlaThrGlnCysSerSerValProGluProArgTyrGlyLys 1504
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 DB 1660 CCCAAATATGCTGTAAACGTAAATCATGTAAACTCTCCAAATCCAGAGATGGGATG 1719
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 DB 2326 -----TCACCGGCGCAAGAGTTTCAAGCTGTGAGCCCGG 2364
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 DB |||||:::|||||
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 DB 2419 CTTGACGCCCCCAACATGAAATCTGTGATGACTTCAATGAGGCCCACTTTTAAT 2478
 QY 1908 GlyThrValITyrSerProGlyPheProSerProTyrSerSerSerGlnAspCysValITrp 1927
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 QY 1928 LeuIleThrValProIleGlyHisGlyValArgLeuAsnLeuSerLeuGlnIThrGlu 1947

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Qy 1968 ValPheThrArgSerMetAlaLysLeuThrValGlnSerSerSerAsnGlnValLeu 1987
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Qy 1988 LysPheHisArgAspAlaAlaThrGlyGlyIlePheAlaIleAlaPheSerAlaTyrPro 2007
Db 2584 -----GCTGGAATGGAAGCCTTGGAAATGACAGTTTCA 2619
Qy 2008 LeuThrLys-----CysProProThrIleLeuProAsnAlaGluValAlaThr 2024
Db 2620 GTGTGTGAACAATCTTTGTCCAAAGTCTCCAGTTATCTTAATGGGAGACACACAGA 2679
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Db 2851 CACTGTCAAGC----- 2862
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Qy 2170 AlaTyrAsnArgGlyGlyPheLysIleArgTyrSerAlaProTyrCysSerLeuProArg 2189
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Db 3052 GATCCAGGAATGGATGTCATGTGATGCACAGACATCCAGTTGATTCAGAAATCAAC 3111
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Qy 2298 -----AsnArgAsnValProPro----- 2303
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Db 3469 TTGATATGACAACAGAACTTATTTCTTAATGAATGAGTTGACATTAGGTGACAG 3528
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Db 3529 CTTGGCTTTGTATGAAGAAGACCCCGCGGTGAGTGAAGTGCAGCGCCCTGAACAAATGGAG 3588
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Qy 2530 GlnCysLeuAlaSerGlyGlnTyrPheSerAspMetLeuProThrCysArgIleIleAsnCys 2549
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Dy      3753  TGtGCTTGCTGGCTGGAATGAAA---GCCCTTGGAATAGCAGTGTTCAGCTGTGTAACA 3809
Oy      2848  LeuMetCYsLYsProProProLeuLeuLeuProAnGlyLYsValValGlySer----- 2864
Dy      3810  ATCTTTGTTCMAATTCCTCCAGCTATCCTTATGGGAGACACAGAGAACTCCTTTGGA 3869
Oy      2865  AspPheMetTrpJlySerSerValThrYrYalCYs----- 2876
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Dy      3987  GGGGTGTGGACAGCCCTGCCCTCTGCTGTGAATCTTGTCTCTGCTGCCCTCCACAT 4046
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Dy      4275  GTATATCACTATGTGAGATTATGTGACTTTCGAAGTGTGAAGATGGGTATATCTCGAAGGC 4334
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Dy      4335  AGTCCCTGGAGCCAGTGCAGGCGGATGACAGATGGAGC-----CTCTCT 4379

RESULT_9
5472939-3
:Patent No. 5472939
:APPLICANT:PEARON, DOUGLAS T.;KLICKSTEIN, LLOYD B.;WONG,
:WINNIE W.;CARSON, GERALD R.;CONCINO, MICHAEL F.;IP, STEPHEN
:H.;NAKRIDES, SAVVAS;MARSH, HENRY C., JR.
:TITLE OF INVENTION: METHOD OF TREATING COMPLEMENT
:MEDATED DISORDERS
:NUMBER OF SEQUENCES: 30
:CURRENT APPLICATION DATA:
:APPLICATION NUMBER: US/08/138, 825
: FILING DATE: 19-OCT-1993
: PRIOR APPLICATION DATA:
:APPLICATION NUMBER: 588, 128
: FILING DATE: 24-SEP-1990
:APPLICATION NUMBER: 412, 745
: FILING DATE: 26-SEP-1989
:APPLICATION NUMBER: 332, 865
: FILING DATE: 03-APR-1989
:APPLICATION NUMBER: 176, 532
: FILING DATE: 01-APR-1988
:SEQ ID NO.:3
:LENGTH: 5420
:472939-3

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Percent Similarity:	34.89%	Conservative:	197	
Best Local Similarity:	23.41%	Mismatches:	620	
Query Match:	6.67%	Indels:	498	
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Db 2943 TCTTGAATGAAGGTTTCCATCTATGTTCCCACTTCTACTTCTCTGCTCAGGC 3002
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Qy 2599 -----ThrTPAAspArgProArgProGlnCysLeuLeuValSerCysGlyHisPro 2615
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Db 3003 AATAATGTCACTGATTAAGAAGGACCTATTTGTGATCATATATCTGT----- 3053
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Qy 2616 GlySerProProHisSerGlnMetSerGlyAspSerTyThr----- 2629
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Db 3054 ---GAGCACCTCCCAACCATATCCAAATGAGACTTCTACAGCAATAGAACATCTTTT 3110
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Qy 2630 ---ValGlyAlaValIleArgTySerCys----- 2638
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Db 3111 CACATATGAACGGTGTACTTACCAGTCCACCTGACCACTGACAGATGAGAACAGCTGTTT 3170
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Qy 2639 -----IleGlyLysArgThrLeuValGlyAsnSerThrArgMetCysGlyLeuAspGly 2656
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Db 3171 GAGCTGTGGGAGAACGGTCAATATAT-----TGACCAAGCAAAAGATGATCAAGTTGGT 3224
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Qy 2657 HisTrpThrGlySerLeuProHisCysSerGlyThrSerValGlyValCysGlyAspPro 2676
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Db 3225 GTTGGAGCAGCCCTCCCTCGGTGATTTCTACTAT-----AATATGACAGCTCCA 3278
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Qy 2677 GlyIleProAlaHisGlyIleArgLeuGlyAspSer-----PheAspProGlyThr 2693
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Db 3279 GAACTT---GAAATATGCAATTAGAGTACCGAGAAACAGAGTTTCTTTCCCTACTGAG 3335
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Qy 2694 ValMetArgPheSerCysGluAlaGlyHisValIleuArgGlySerSerGluArgThrCys 2713
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Db 3336 ATCATCATGATTTAATGATGTACGCCCGGTTTGTCTATGAGAGGTCCACACATGTCAGTGC 3395
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Qy 2714 GlnAlaAsnGlySerTrpSerGlySerGlnProGlyCysGlyValIleSerCysGlyAsn 2733
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Db 3396 CAGACCAATGCGCAATGGGGCCCAAGCTGCACTGCTCCAGGAG---TGTCAAGCCG 3452
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Qy 2734 ProGlyThrProSerAsnAlaArgValIlePheSer-----AspGlyLeuValPheSer 2751
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Db 3453 CTTCCAGAAATCTCGATGTGAGCATACCTTAAGCCATGACAGACAATTTTCACTGGG 3512
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Qy 2752 SerSerIleValIleGlyCysArgGlyGlyTyThrAlaThrGlyLeuLeuSerArgHis 2771
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Qy 2772 CysSerValAsnGlyThrTrpThrGlySerAspProGluCysLeuValIleAsnCysGly 2791
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Db 3573 TGACGCCCCAGGAGACCTGAGCCCTGAAAGCCCTTAAGATGTACAGTGAATCTGTGAT 3632
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Qy 2792 Asp-----ProGlyIleProAlaAsnGlyLeuArgLeuGlyAsnAspPheArgTyAsn 2809
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Db 3633 GACTTCTGGGCCCACTCCCTCATGCGCGTGTCTACTTCCATTAATCCAGCTTGGG 3692
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Qy 2810 LysThrValThrTyGlnCysValProGlyTyMetMetGlnSerHisArgValSer--- 2828
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Db 3693 GCAAGGTGCTCTTGTGCGATGAAGGGCTCGATTAAAGCAGAGTCTGTATGCAT 3752
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Qy 2829 ---ValLeuSerCysThrLysAspArgThrTrpAsnGlyThrLysProValCysLysAla 2847
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Qy 2848 LeuMetCysLysProProLeuIleProAsnGlyLysValIleGlySer----- 2864
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Qy 2877 -----LeuGlyGlyTyGlnLeuSerLeuProAlaValPheThrCysGlyLysAsn 2893
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Db 3930 ACCTTCAACTCATTTGGG---GAGAGCTCATCCGCTGCACAAAGTGAACCTCAAGGAGAT 3986
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Qy 2894 GlySerTrpThrGlyGlyLeuLeuProGlnCys-----PheProValPheCysGlyAsp 2910
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Db 3987 GGGGTTTGGAGCAGCCCTGCGCTCGTGAACCTTCTGCTGCTGCTGCCCAT 4046
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Qy 2911 ProGlyValProSerArgGlyArgArgGlyAspArgGlyPheSerTy-----Arg 2927
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Db 4047 CCACCCAGATCCCAAAACGGGGCATTTACATTGAGAGACACCTATCTATATCTTCTGGG 4106
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Qy 2928 SerSerValSerPheSerCysHisProProLeuValIleValGlySerProArgArgPhe 2947
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Db 4107 ATGACATATCAGTACCTTGTGACCCCGGCTACTGTGATGAGAAAGGCTTCATTTTC 4166
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Db 4218 AATTGTAGCTTCCCA---CTGTTATGAATGGAATCTCGAAGAGATTAGAAATGAAAAA 4274
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Qy 3005 SerThrThrArgThrCysLeuProAsnLeuThrTrpSerGlyThrProPro 3021
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Db 4335 AGTCCCTGGAGCCAGTCCAGGGGAGTACAGATGGGAC-----CCTCCT 4379
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RESULT 10

US-09-023-655-1066

Sequence 1066, Application US/09023655

Patent No. 6607879

GENERAL INFORMATION:

APPLICANT: Cocks, Benjamin G.

APPLICANT: Susan G. Stuart

APPLICANT: Jeffrey J. Sellhammer

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE EXPRESSION

Db 1000 GAAGAGTGAACCTTATGAGAGACACTCCGTTGTATAGTATAGTAC 1059
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Qy 2419 -----GlyLeuThrProGlySerGlyValArgCys-----LeuAlaGlyHis 2432
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Qy 2433 CysGlyThrProGlyProIleValAsnGlyHisIleAsnGly-----GluAsnTyrSer 2450
Db 1120 TGTCCACATCCCCGATCTTAAGAGCCGAATGATCTGGCAGAAAGATTCGATATACC 1179
Qy 2451 TyrArgIleSerValValTyrGlnCysAsnAlaGlyPheArgLeuIleGlyMetSerVal 2470
Db 1180 TATAAGACACCTGATATTGCTTGCATGTTTGGCTTACCTTGAAGGGAGACAGACCA 1239
Qy 2471 ArgIleCysGlnIleAspHisIleTyrSerGlyLysThrProPheCysValProIleThr 2490
Db 1240 ATCCGATGCAATGCCCAAGGACATGGGAGCCATCTCACACAGTCTGAAAG---GAA 1296
Qy 2491 CysGlyHisProGlyAsnProValAsnGlyLeuThrGlnIleAsn-----GlnPhe 2507
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Qy 2508 AsnLeuAsnAspValValIysPheValCysAsnProGlyTyrMetAlaGlnIleValAla 2527
Db 1357 GACCCCTGGAACATCTAATAAATATAGCTGTAACTTGGCTATGCTGCTGGAGAGAA 1416
Qy 2528 ArgSerGlnCysIleValAsnGlyGlnTyrSerAspMetLeuProThrCysArgIle 2547
Db 1417 TCCATACAGTACCTCTGAGGGGGTGTGGACCCCTGTACCCCAATCCAAATGGCA 1476
Qy 2548 AsnCys-----ThrAspProGlyHisGln----- 2555
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Qy 2556 -----GluAsnSerValArgGln----- 2561
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Qy 2561 ----- 2561
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Qy 2562 -----ValHisAlaSerGlyProHisArg-----PheSerPheGly 2573
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Qy 2574 ThrThrValSerTyrArgCysAsnHisGly-----PheTyrLeuLeu 2587
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Qy 2604 ArgProGlnCys-----LeuLeuValSerCysGlyHisProGlySerPro 2619
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Qy 2620 HisSerGlnMetSerGlyAspSer-----TyrThrValGlnAlaValAlaArgTyrSer 2637
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Qy 2638 CysIleGlyLysValArgTyrLeuValGlyAsnSerThrArgMetCysGlyLeuAspGlyHis 2657
Db 1957 TGTATAGTGGATTACTTGAAGGAGAGTAGTCAAGTGGTCTTCAAGAGGTAAACACC 2016
Qy 2658 TyrThrIleLysLeuProHisCysSerGlyThrSerValGlnValCysGlyAsp----- 2675
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Qy 2676 -----ProGlyIleProAlaHisGlyIleArgLeuGlyAspSerPheAspProGly 2692
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Db 2068 CAGAGTCTTCAAGAACTTCCAGCT---GGTTCACTGTG----- 2103
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Qy 2713 CysGln-----AlaAsnGlySerTyrSerGlySerGlnProGlyLysGlyValIleSer 2730
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Qy 2731 CysGlyAsnProGlyThrProSerAsnAlaArg-----ValValPheSerAspGlyLeu 2748
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Qy 2749 ValPheSerSerIleValTyrGlnCysArgGlnGlyTyrTyrAlaThrGlyLeuLeu 2768
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Qy 2769 SerArgHisCys-----SerValAsnGlyThrTyrThrGlySerAspProGly 2784
Db 2344 AATTTCAGTGCAGAAATGATTTTAAAGACATGATCTTGGAGCGGCTTCCACAG 2403
Qy 2785 CysLeu-----ValIleAsnCysGlyAspProGlyIleProAlaAsnGlyLeu 2800
Db 2404 TGTTCAGATCTCTCTGCTGTGATCGCTGCTTAATCCAGAGTCT---AAACATGGGTAC 2460
Qy 2801 ArgLeuGly-----AsnAspPheArgTyrAsnLysThrValThrTyrGlnCysVal 2817
Db 2461 AACCTCAATMAAACATTTGCTATTTCCCAACAAAGACATAGTGTATGTGACTGMA 2520
Qy 2818 ProGlyTyrMetMetGluSerHisArgValSerValLeuSerCysThrLysAspArgThr 2837
Db 2521 CTGGCTTCATCATGATGTAGTACTGCG-----GTGATTTGGTGTCTACTGTATACACA 2574
Qy 2838 TyrAsnGlyThrLysProValCys-----LysAlaLeuMet---CysLysProProPro 2854
Db 2575 TGGGTGCAGAGTGTGCCAATCTGTATGAAAAGCCCTTACAGAGTGTCCACCTCGCCT 2634
Qy 2855 LeuIleProAsnGlyLysValValGlySerAsp-----PheMetTyrGlySerSer 2871
Db 2635 AAGACCCCTAAACGGAAACCATCTGGTGGAAACATAGCTGATTTCTCTCGAAGTCA 2694
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Qy 2928 SerSerValSerPheSerCysHisProProLeuValLeuValGlySerProAlaArgPhe 2947
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Db 3026 TTCTTACTTCTTGAATGTGATTAACCTTATACGTGATATCAAAACACAGAGAAAGCAAT 3085
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QY      3003 GlnGlySerThrThrArgThrCysLeuProAsnLeuThrTrpSerGlyThrProProAsp 3022
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QY      3023 CysValProHis 3026
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RESULT 11
US-09-285-385C-3
; Sequence 3, Application US/09285385C
; Patent No. 6579702
; GENERAL INFORMATION:
; APPLICANT: Greenspan, Daniel S.
; APPLICANT: Scott, Ian C.
; APPLICANT: Thomas, Christina L.
; TITLE OF INVENTION: MAMMALIAN TOLLOID-LIKE GENE AND PROTEIN
; FILE REFERENCE: 960296.9611
; CURRENT APPLICATION NUMBER: US/09/285,385C
; PRIORITY FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/111873
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: 60/080550
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 4661
; TYPE: DNA
; ORGANISM: mouse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (191)..(3229)
US-09-285-385C-3

Alignment Scores:
Pred. No.: 7.5e-49 Length: 4661
Score: 779.50 Matches: 344
Percent Similarity: 36.69% Conservative: 206
Best Local Similarity: 22.95% Mismatches: 508
Query Match: 4.59% Indels: 445
DB: Gaps: 55

US-10-016-248-2 (1-3104) x US-09-285-385C-3 (1-4661)
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DB      284 GCCTTGACATAAGGA-----GCCTTG 304
QY      1062 GluAlaGluAlaGlyCysThrIleGlyLeuHisPheLeuValPheAspThrGluGluVal 1081
DB      305 GAAGGGGAGAGGAGCGACGAGACAGCTGCTATTAC----- 340
QY      1082 HisAspValLeuArgIleTPrAspGlyProValGlnSerGlyValLeuLeuGlnLeu 1101
DB      341 CACGAC-----CCCTGCAAGCTGCTGCTTCTTGGGGAGATATT 379
QY      1102 SerGlyProAlaLeuProGlyAsp-LeuHisSerThrPheAsnSerValValLeuGlnPhe 1121
DB      380 -----GCTGTGATGAAGATGATCTCAAGTTATTTCACATCCACAAGGCTTGAGAC 430
QY      1121 eSerThrAspPhePheThrSerIleGlnGlyPheAlaIleGln-PheSerValSerThr 1140
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QY      1141 AlaThrSerCysAsnAspProGlyIleProGlnAsnGlySerArgSerGlyAspSerTrp 1160
DB      491 GCAAGTGGCCAAACGATACAGCC-----TTTAAAGCCAGCATCCAGGACCAAGAAAG 544

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QY      1181 GluIleSerCysValIleGlnAsn----- 1189
DB      604 GACCTTCTGCTCGAGTTGGAAGAGCTCAACCTCAAGACAGAGCGATTGGCCTGG 663
QY      1190 -----ArgPhePheThrGlnProSerProProThrCys 1200
DB      664 AGGGTCATTCCTTATGTCATTGAGAGAACTTACTGTGTACCAAGAGG-CCATTTCGA 722
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DB      783 AGGAAAGCTTCATTGATTCAAGTACAGGACCT-----GTGGTGTGTCTCTACGTGG 836
QY      1221 Pro-----GluProTyrProProGlyLysGluCysAsp----- 1231
DB      837 GAGCCCGAGAGGTGGCCGCGACGCTATATCCATC-GGGAAAACTGTGACAAATTCCGC 895
QY      1232 -----TrpLysValThrValSerProAsp 1239
DB      896 ATTGGGCTCAGAGCTGGGCACTGTGGTGGTCTGTGCAAGAACACACTGGCCAGAC 955
QY      1240 TyrValIleAlaLeuValPheAsnIlePheAsnLeuGluProGly-----TyrAspPhe 1257
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DB      1097 TTCTCA-----AGAGAGTTTCTTTAGAC--ACCATCCTCCCGCTGAGAC-- 1141
QY      1318 PheAspProGlySerIleLysAsnGlyThrArg-----ValGlySerAspLeuLysLeu 1335
DB      1142 -----GACATGGCGCTCAGGCCAACCATTTGGCCAAACGCTGGGCTTC 1183
QY      1336 GlySerSerValThrTyrCysHisGlyGlyTyrGluValGluGlyThrSerThrLeu 1355
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QY      1356 SerCysIleLeuGlyProAspGlyLysProValTyrAsnAsnProArgProValCysThr 1375
DB      1223 -----TGCCCA 1228
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QY      1415 ValVal-----PheGlyGlnPheAlaPhePheHisThrAlaLeu-----AsnAspVal 1430
DB      1346 ATCATCTCTAAATTTCACCTCATGATGATTGTTTAAAGACCCGCTGTGCTGATCATAC 1405
QY      1431 ValGluValHisAspGlyHisSerGlnHisSerArgLeuLeuSerSerLeuSerGlySer 1450
DB      1406 GTGGAGATCCGGAGATGTACTGGAGAAAGGCCCTCTGTGGAGAGGTTCTGTGCGCAT 1465

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QY 1451 HisThrGlyLeuSerLeuProLeuAlaThrSerAsnGlnValLeuIleLysPheSerAla 1470
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 QY 1471 LysGlyLeuAlaProAlaArgGlyPheHisPheValTyrGlnAlaValProArgThrSer 1490
 DB 1523 AGCAGACACACCTGGGCAAGAGCTTTGCTGTATATGAAGCCATG----- 1570
 QY 1491 AlaThrGlnCysSerSerValProGluProArgTyrGlyLysArgLeuGlySerAspPhe 1510
 DB 1570 ----- 1570
 QY 1511 SerValGlyAlaIleValArgPheGlnCysAsnSerGlyTyrAlaLeuGlnGlySerPro 1530
 DB 1570 ----- 1570
 QY 1531 GlnIleGlnCysLeuProValProGlyValaLeuAlaGlnTyrPheAsnValSerAlaProThr 1550
 DB 1570 ----- 1570
 QY 1551 CysValValProCysGlyGlyValAsnLeuThrGlnArgArgGlyTyrIleLeuSerProGly 1570
 DB 1571 -----TGTGGGGAGACATACCAAGATGCGAGCGCAGATTCACTCCCAAC 1618
 QY 1571 PheProGluProTyrLeuAsnSerLeuAsnCysValTyrPylsIleValValProGluGly 1590
 DB 1619 TACCTTGACACTACAGACTTCCCAAGGAATGTGTGTGAGAGATACAGTCCCGACGG 1678
 QY 1591 AlaGlyIleGlnIleGlnValValSerPheValThrGlnAlaAsn-----Tyr 1606
 DB 1679 TTCATGTGGGACTTCACTTCACGCTTCAGATTCGAAGACATGACAGTTGTGCAAT 1738
 QY 1607 AspSerLeuGlnValPheAspGlyValaAspAsnThrValThrMetLeuGlySerPheSer 1626
 DB 1739 GACTATCTGGAAATCCGAGGCTCCACAGAGACAGCACCTGATTTGGCAGCTCTGT 1798
 QY 1627 GlyThrThrValProAlaLeuLeuAsnSerThrSerAsnGlnLeuTyrLeuHisPheTyr 1646
 DB 1799 GGCTACGAGAAAGCCGAGGCGGTAAATCCAGCGCTAACCGACTGTGGGTGAAGTTTGT 1858
 QY 1647 SerAspIleSerValSerAlaIleGlyPheHisLeuGlnTyrLysThrValGlyLeuSer 1666
 DB 1859 TCCACGCGCTCCATCAATAAAGCGGCTTTCAGCCCAATTTC-----TTCAG 1906
 QY 1667 SerCysProGluProAlaValProSerAsnGlyValLysThrGlyGlnArgTyrLeuVal 1686
 DB 1907 GAGGTGATGAGTCTCTCGGACAGACCATGTG-----GGATGTGAGCAGCGGTGTGTA 1960
 QY 1687 AsnAspValValSerPhe-----GlnCysGluProGlyTyrAlaLeuGlnGlyHisAla 1704
 DB 1961 AACACACTCGGCACTACACGTGTGCTGTGACCTGTGCTACGAATGGCTGCC----- 2014
 QY 1705 HisIleSerCysMetProGlyThrValArgArgTyrPheAsnTyrProProLeuCysIle 1724
 DB 2015 -----GACAAAGAACATGTGAA 2032
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 DB 2033 GTGGCTGTGTGTGCTTCAATTAACCAAGTAAACGACCATCACAGCCCTGAGTGGCG 2092
 QY 1745 GlnValAsnTyrProSerAsnMetAspCysSerTyrPylsIleAlaLeuProValGlyPheGly 1764
 DB 2093 AAGAGAGATTCACCAACAAAGAACTGTGTCTGGCAGGTGTGTGTGTGTGTGTGTGTGT 2152
 QY 1765 AlaHisIleGlnPheLeuAsnPheSerThrGluProAsn-----HisAspTyr 1780
 DB 2153 ATCTCACTGCACTTCGAAGCCTTGTAGCTGAGAGCAATGACGTGTAGATAGACTTC 2212
 QY 1781 IleGlnIleArgAsnGlyProTyrGlnThrSerArgMetMetGlyArgPheSerGlySer 1800
 DB 2213 GTAAAGGTGGCGAGTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2272
 QY 1801 GluLeuProSerSerLeuLeuSerThrSerHisGlnThrThrValTyrPheHisSerAsp 1820

DB 2273 GAGACCCCGGAGGTATCATCATCCAGAGCAACAACATCGAGTGAATTCAGTCTAC 2332
 QY 1821 HisSerGlnAsnArgProGlyPheLysLeuGlnTyrGlnAlaTyrGlnLeuGlnGlyCys 1840
 DB 2333 AACACCGTCTCAAGCGAGGCTTCAAGGCTCACTTCTTCTTA---GACAAAGACAGAGT 2389
 QY 1841 ProAspProGluProPheAlaAsnGlyIleValArgGlyAlaGlyTyrAsnValGlyGln 1860
 DB 2390 GCCAAAGC-----AATGGCGGCTGCCAGCAGAGGTGTCTACACGTTGGG 2437
 QY 1861 SerValThrPheGlnCysLeuProGlyTyrGlnLeu-----ThrGlnHisPheValLeu 1878
 DB 2438 AGTACCTGTGACATGACAGAGACGGGTACCGATCGATGAGAACGGACAC----- 2488
 QY 1879 ThrCysGlnHisGlyThrAsnArgAsnTyrAspHisProLeuProLysCysGlnValPro 1898
 DB 2489 GACTGCAAA-----GAGGCTGGC 2506
 QY 1899 CysGlyGlyAsnIleThrSerSerAsnGlyThrValTyrSerProGlyPheProSerPro 1918
 DB 2507 TCGCCCTTCAAGATCAGCAGTGCAGAGGGGACCTGTATGACTCTTAACCTGGCAGACAA 2566
 QY 1919 TyrSerSerSerGlnAspCysValTyrPylsIleThrValProIleGlyHisGlyValArg 1938
 DB 2567 TACCCAGCCGGAAGAAATGTACTGTGAACATTTCATCAACCGACGCGCAAGGGTGA 2626
 QY 1939 LeuAsnLeuSerLeuLeuGlnThrGluPro-----SerGlyAspPheIleThr 1954
 DB 2627 ATTACATTCAGTGTGCTCGAGATTGACAGACAGCAAGATGTGCTTGTGACCACTGGAA 2686
 QY 1955 IleTyrAspGlyProGlnGlnThrAlaProArgLeuGlyValPheThrArgSerMetAla 1974
 DB 2687 CTGTACATGTGAGACAGACAGCTTGGCCCATCTTGTGCGCTTGTGCGGAGAGAG 2746
 QY 1975 LysIleThrValGlnSerSerSerAsnGlnValLeuLeuLysPheHisAspAlaAla 1994
 DB 2747 CCGGATCCCGTGTGGGAGCAGGACGACGACGATATCTCACTTACCTGCGAGCGCTCA 2806
 QY 1995 ThrGlyGlyIlePheAlaIleAlaPheSerAlaTyrProLeuThrLysCysProPro 2014
 DB 2807 -----GTGACCGCGAAAGCTTCCAGGCTGTGACAGCAGACAGATG- 2848
 QY 2015 ThrIleLeuProAlaAlaGlnValValThrGlnAsnGlnGluPheAsnIleGlyAspIle 2034
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 QY 2035 ValArgTyrArgCysLeuProGlyPheThrLeuValGlyAsnGlnIleLeuThrCysLys 2054
 DB 2849 -----GGGGCAGGCTGAAGCT---GAAGTACAGACCAAGAG 2884
 QY 2055 LeuGlyThrTyrLeuGlnPheGlnGlyProProIleCysGlnValHisCysProThr 2074
 DB 2885 CTCTATTCCCATGCCAGTTTGGG----- 2908
 QY 2075 AsnGlnLeuLeuThrAspSerThrGlyValIleLeuSerGlnSerTyrProGlySerTyr 2094
 DB 2909 -----GACAAACACTAC 2920
 QY 2095 ProGlnPheGlnThrCysSerTyrPylsValArgValGluProAspTyrAsnIleSerLeu 2114
 DB 2921 CCGAGCAGGCGCGCTGTGACTGGGTATGTGGCAGAAAGCGTTATGGCGTGAAGCTG 2960
 QY 2115 ThrValGlnTyrPheLeuSerGlyLysGln-----TyrAspGlnPheGlnIle 2130
 DB 2981 ATATTCCGACCTTTGAAGTTGAGAGAGAGAGTACTGTGGCTACGACTTCATGAGAGCT 3040
 QY 2131 PheAspGlyProSerGlyGlnSerProLeuLeuValAlaLeuSerGlyAsnTyrSerAla 2150
 DB 3041 TATGATGGTACAGACAGACTGGACCCAGGCTGGCGCTTCTGTGTGC-----TCAGG 3094
 QY 2151 ProLeu---IleValThrSerSerSerAsnSerValTyrLeuArgTyrPheSerSerAspHis 2169

Db 1314 ---GAATCCAAATGCGCAACTTTCTCTCCAGATTTCCTCAATGCGTCACTCTTTACACA 1370
 Qy 1056 AsnCysValIetPrpThrIleGluAlaGluAlaGlyCysThrIleGlyLeuHisPheLeuVal 1075
 Db 1371 CACGCAATCTGGAGAGTTTCTGTGACCCCGAGGAGGAAGATGTTTAAATTTTACACG 1430
 Qy 1076 PheAspThrGluGluVal-----HisAspValIleuArgIleTPAspGlyPro 1091
 Db 1431 ATGATATCTAATCAAGAGTAGTTTGTCTGTGATATCTAATATGAAAGTAAGACGGGTAC 1490
 Qy 1092 ValGluSerGlyValIleuLeuGlyGluLeuSerGlyProAlaLeuProGlyAspLeuHis 1111
 Db 1491 TGGAAATATCACCTCTCTGTGATGAGATTCTGGGACAAATGCTGGAAGTTCTTACT 1550
 Qy 1112 SerThrPheAsnSerValValIleuGlnPheSerThrAspPheThrSerIleGlyGlnGly 1131
 Db 1551 TCTACACACAGCAGAAATGTGATGAGTTT----- 1580
 Qy 1132 PheAlaIleGlnPheSerValSerThrAlaThrSerCysAsnAspProGlyIleProGln 1151
 Db 1580 ----- 1580
 Qy 1152 AsnGlySerArgSerGlyAspSerIleProGluAla---GlyAspSerThrValPheGlnCys 1170
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 Qy 1231 AspTyrIleValIleThrValSerProAspTyrValIleAlaLeuValPheAsnIlePheAsn 1250
 Db 1716 GTGGGAAATTAACAGTGTGAGAGCTACCACTGCGGCTGACCTTTCAGCTCTTGAG 1775
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 Db 1776 ATTTAAAGACATGACAAATTGCTTATGACTGAGAGTTAGAGATGGAACCACTGAA 1835
 Qy 1267 LeuSerProLeuIleGlySerPheTyrGlySerGlnLeuProGlyArgIleGluSerSer 1286
 Db 1836 AATAGCCCTTTGATAGGCGCTTCTGTGTTATGACAAACCTGAAAGCATTAAGTCTAAC 1895
 Qy 1287 SerAsnSerLeuPheLeuAlaPheArgSerAspAlaSerValSerAsnAlaGlyPheVal 1306
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 Qy 1307 IleAspTyrThrGluAsnProArgGluSerCysPheAspProGlySerIleGlyAsnGly 1326
 Db 1956 GCTAACTTTTAAAGAG---GAAGATGAGTGTCCAACT----- 1994
 Qy 1327 ThrArgValGlySerAspLeuLeuGlySerSerValThrTyr-----Cys 1343
 Db 1995 GACCTGAGGCTGTGACGACCAATGTCTGAACCTGCGGCACTTACACTGCGCTGT 2054
 Qy 1344 HisGlyGlyTyrGluValGluGlyThrSerThrLeuSerCysIleLeuGlyProAspGly 1363
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 Qy 1364 LysProValIleTyrAsnAsnProArgProValCysThrAlaProCysGlyGlyGlnTyrVal 1383
 Db 2082 -----AGAAGAGCTGTGAACCTGCTGTGTGTGAGCTTCTTACC 2120
 Qy 1384 GlySerAspGlyValIleLeuSerProAsnTyrProGlnAsnTyrThrSerGlyGlnIle 1403
 Db 2121 AAATTTAAGCGCACCATTAACACCCCTGCTGCGCCCAAGAGTACCTCTCTAATTAAGAC 2180

Qy 1404 CysLeuTyrPheValIleThrValProGlyAspTyrValValPheGlyGlnPheAlaPhePhe 1423
 Db 2181 TGTGTGTGCAATGTGTGACCAACCACTGACAAATTTCTGTGAAGTTTGATTTT 2240
 Qy 1424 HisThrAlaLeuAsnAspVal-----ValGluValHisAspGlyHisSer 1438
 Db 2241 GAATTTGAAGCAATAGCGTTTGCAAAATATGATTATGTGAGATCTGAGAGTGTCTTCC 2300
 Qy 1439 GlnHisSerArgLeuLeuSerSerLeuSerGlySerHisThrIleGlyLeuSerProLeu 1458
 Db 2301 TCTGAGTCTTAACCTGATGCAAAATTTCTGTGCGCTGAGATGCTCAAGATGATC---ACA 2357
 Qy 1459 AlaThrSerAsnGlnValIleuPheSerAlaIleGlyLeuAlaProAlaArgGly 1478
 Db 2358 TCCAGTTCACAAATATGAAATTAATTAATCTGACATATCTGATTCAGAAAGGCG 2417
 Qy 1479 Phe-----HisPheValTyrGlnAlaValProArgThrSerAlaThrGlnCysSerSer 1496
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 Qy 1497 ValProGluProArgTyrGlyIleArgLeuGlySerAspPheSerValGlyAlaIleVal 1516
 Db 2457 ---AAGGATATGCTGATGTGACAGCAATGTGTCAACAGATGGGAGCTATAGT 2510
 Qy 1517 ArgPheGluCysAsnSerGlyTyrAlaLeuGlnGlySer-----ProGluIle 1532
 Db 2511 ---GTCAATGCGGTAAATGATTTGTCTACATGACATTAACATGATTCAGAAAGCT 2567
 Qy 1533 GluCysLeuProValProGlyAlaLeuAlaGlnTyrAsnValSerAlaProThrCysVal 1552
 Db 2568 GAGTGT-----GAACAGAAAGTCCACAGTCCAACT----- 2597
 Qy 1553 ValProCysGlyGlyAsnLeuThrGluArgArgGlyThrIleLeuSerProGlyPhePro 1572
 Db 2598 -----GGCCTCATCACAGTCCCACTGCGCCA 2624
 Qy 1573 GluProTyrLeuAsnSerLeuAsnCysValTyrIleValIleValProGluGlyAlaGly 1592
 Db 2625 GACAGATGCCAAGCAGAAAGAAATGACATTTGGGAAATCGCCCACTCTGCGCCAGA 2684
 Qy 1593 IleGlnIleGlnValValSerPheValThrGlnGlnAsn-----TyrAspSer 1608
 Db 2685 ATCAAAATTAACCTTTAGTGAATTTGAGATTGAGACAGCATTAAGATGCTTATGACAC 2744
 Qy 1609 LeuGluValPheAspGlyAlaAspAsnThrValThrMetLeuGlySerPheSerGlyThr 1628
 Db 2745 TTGAAGTATTTGATGAGAAACAGAAAGTCAACCATTTCTGACGACTATGTGCGAAC 2804
 Qy 1629 ThrValProAlaLeuLeuAsnSerThrSerAsnGlnLeuTyrIleHisPheTyrSerAsp 1648
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 Qy 1649 IleSerValSerAlaIleGlyPheHisIleuGluTyrIleThrValGlyLeuSerSerCys 1668
 Db 2865 GCATCTGTTTAAAGAAAGGCTTTCAAGCCACATTTTCA----- 2306
 Qy 1669 ProGluProAlaValProSerAsnGlyValIleThrGlyGluArgTyrLeuValAsnAsp 1688
 Db 2906 ----- 2906
 Qy 1689 ValValSerPheGlnCysGluProGlyTyrAlaLeuGlnGlyHisAlaHisIleSerCys 1708
 Db 2906 ----- 2906
 Qy 1709 MetProGlyThrValArgArgTyrAsnTyrProProProLeuCysIleAlaGlnCysGly 1728
 Db 2907 -----GAGTGTGCG 2915
 Qy 1729 GlyThrVal-----GluGluMetGluGlyValIleLeuSerProGlyPheProGly--- 1745
 Db 2916 GAGCAATTGAACAGATTAACAAACCAAGAGATCTGTACTCAATGCTGAGTTGGTAT 2975

QY 1746 ---AsnTYrProSerAenMetAspCysSerTrpIleAlaLeuProValGlyPheGly 1764
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 QY 1765 AlAHsileglInPheLeuAenPheSerThrGluPro-----AenHsAspTYr 1780
 DB 3036 CTGAATATTCCTCCAGACATTTGAAGTAGAGAGAGACGAGCTGTGCTATGACTAT 3095
 QY 1781 ILGLuIleArgAenGlyProTYrGluThrSerArgMetGlyArgPheSerGlySer 1800
 DB 3096 GTGAGGCTCTTTGATGGCTCTTGATTCACAGCTGTGGCTGGCTGCTGATTCGATCC 3155
 QY 1801 GluLeuProSerSerLeuLeuSerThrSerHsileglInThrValTYrPheHsSerAsp 1820
 DB 3156 GGGCCACCAAGAGATTTTCAATTCGATTCGAGATTCAGTTTCAATTCATTCCTCCACTGAT 3215
 QY 1821 HsSerGluAenArgProGlyPheLeuGluTYrGlnAla 1834
 DB 3216 GACACATCAACAAAGAGGATTCATATAGATACAAAGC 3257

RESULT 13

US-09-432-473-1
 ; Sequence 1, Application US/09432473
 ; Patent No. 6365715
 ; GENERAL INFORMATION:
 ; APPLICANT: ARLETTE, ANTHONY J.
 ; APPLICANT: WILLETTTE, ROBERT N.
 ; APPLICANT: ELISHOURBAGY, NABIL A.
 ; APPLICANT: LI, XIAOTONG
 ; TITLE OF INVENTION: HUMAN CARDIAC/BRAIN TOLLITD-LIKE PROTEIN
 ; FILE REFERENCE: ATG-50038-D1
 ; CURRENT APPLICATION NUMBER: US/09/432,473
 ; EARLIER FILING DATE: 1999-11-01
 ; EARLIER APPLICATION NUMBER: 08/991,408
 ; EARLIER FILING DATE: 1997-12-16
 ; EARLIER APPLICATION NUMBER: 60/034,471
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 5145
 ; TYPE: DNA
 ; ORGANISM: HOMO SAPIENS
 ; US-09-432-473-1

Alignment Scores:

Pred. No.: 5,1e-48 Length: 5145
 Score: 769.50 Matches: 245
 Percent Similarity: 37.83% Conservative: 131
 Best Local Similarity: 24.65% Mismatches: 331
 Query Match: 4.53% Indels: 287
 DB: 3 Gaps: 33

US-10-016-248-2 (1-104) x US-09-432-473-1 (1-5145)

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 QY 899 AlaArgAlaPheGluLeuSerGluGlyAspValLeuLYrArgGlyAenAenAen 918
 DB 1068 -----GAGTACAATTTTCTGAAGATGGAGCCTGGAGCAAGCAAGC 1106
 QY 919 SerAlaArgLeuLeuGlyVal---PheSerHsileglInMetGlyValThrLeuAen 937
 DB 1107 TCA-----CTTGAGAGAAAGATATGATTTGACAGATATCATATGCCAGCAAGC 1157
 QY 938 SerThrSerSerLeuLeuTrpLeuAspPheileThrAspAlaGluAenThrSerLysGly 957
 DB 1158 ACCTTCTCAAGGGGAGATGTTCTGATACCATTTCTCCCTCCGCT----- 1202
 QY 958 PheGluLeuHsilePheSerSerPheGluLeuileLysCysGluAspProGly---ThrPro 976

DB 1203 -----GATGATATATGCACTAGCTCT 1223
 QY 977 LysPheGlyTYrLysValHis---AspGluGlyHsPheAlaGlySerSerValSerPhe 995
 DB 1224 GCATTTGTGCAAGCAACCCGCTTAAGCAAGAGATATGCAAGCA----- 1271
 QY 996 SerCysAspProGlyTYrSerLeuArgLysSerGluLeuLeuLysSerGlyGlu 1015
 DB 1271 ----- 1271
 QY 1016 ArgArgThrTrpAspArgProLeuProThrCysValAlaGluCysGlyGlyThrValArg 1035
 DB 1272 -----AGAAAGCTGATAGATGCTCAGCA---TGCGAGAAAGCTTCACAA 1313
 QY 1036 GlyGluValSerGlyGlnValLeuSerProGlyTYrProAlaProTYrGlnHsAenLeu 1055
 DB 1314 ---GAATCAATGGAACCTTTCCTCCAGAGATTTCCCAATGGCTTCTTACACA 1370
 QY 1056 AenCysileTrpThrileglInAlaGluAlaGlyCysThrileglInLeuHsPheLeuVal 1075
 DB 1371 CACTGCATCTGAGAGAGTTTCTGTGACCCAGGGAGAAAGATTTTAAATTTTACACG 1430
 QY 1076 PheAspThrGluLysVal-----HsAspValLeuArgileTrpAspGlyPro 1091
 DB 1431 ATGATCTATACAAAGAGTAGTTTGCTGTGATGACTATATGAAGTAAAGACGGGTAC 1490
 QY 1092 ValGluSerGlyValLeuLeuLysSerGlyProAlaLeuProLysAspLeuHs 1111
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 DB 1551 TCTACAGACAGAGAAATGAGATTGATTT----- 1580
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 DB 1628 ----- 1628
 QY 1191 PhePheTrpGlnProSerProProThrCysileAlaProCysGlyLysAspLeuThrGly 1210
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 QY 1211 ProSerGlyValileLeuSerProAenTYrProGlyProTYrProProGlyLysGlyCys 1230
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 QY 1251 LeuGluPro-----GlyTYrAspPheLeuHsileTYrAspGlyArgAspSer 1266
 DB 1776 ATTTGAAGACATGACAAATTTGCTTATGACTACCTGGAAGTATGAGATGAACCAAGTGA 1835
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 QY 1307 IleAspTYrThrGluAenProArgGluSerCysPheAspProGlySerileLysAenGly 1326
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QY 1327 ThrArgValGlySerAspLeuLeuGlySerSerValThrTyr-----Cys 1343
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 DB 1395 GACCTGGAGGCTGTGTGACGACGATGCTGAACTCTGGGCACTTCCAGTCGCTGT 2054
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 DB 2055 GAGCTGGCTATGAG-----CTGGGCCCAAGAC--- 2081
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 DB |||||
 DB 2121 AAACCTTAACGGCCACCATACCACTGCTGGCTGGCCCAAGAGTACCTCTTAATTAAGAC 2180
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 DB 2181 TGTGTGTGCAAGTGTGTGCAACCAACGATACAGAAATTTCTGTGAAGTTGAGTTT 2240
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 QY 1459 AlaThrSerArgGlnValLeuIleLysPheSerAlaLysGlyLeuAlaProAlaArgGly 1478
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 DB 2418 TTCAAGACACATTTTTC-----TCAGCAAAAGATGATGCTCT--- 2456
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 DB |||||
 DB 2457 -----AAGGATTAATGTGATGTGACGACGAAATGTGTCAACAGATGGGAGTACATG 2510
 QY 1517 ArgPheGlyCysAsnSerGlyTyrAlaLeuGlnGlySer-----ProGlnIle 1532
 DB |||||
 DB 2511 ---TGTCAATGCGTAATGATGATTTGTGCTACATGCAATTAACATGATGCAAGAACT 2567
 QY 1533 GluCysLeuProValProGlyAlaLeuAlaGlnTyrPheValIleSerAlaProThrCysVal 1552
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 DB 2568 GAGGT-----GACAGAAAGATCCACAGTCCAAAGT----- 2597
 QY 1553 ValProCysGlyGlyAsnLeuThrGluArgArgGlyThrIleLeuSerProGlyPhePro 1572
 DB |||||
 DB 2598 -----GGCCCTCATCCACAGTCCCAACGTGGCA 2624
 QY 1573 GluProTyrLeuAsnSerLeuAsnCysValTrrLysIleValValProGlnGlyAlaGly 1592
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 DB 2625 GACAAATGCCAAGAGGAAAGAAATGCACTTGGGAAATCAGCCCACTCTGGCCACCGA 2664
 QY 1593 IleGlnIleGlnValIleSerPheValThrGlnAsn-----TrpAspSer 1608
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 DB 2805 AAGATACCAAGATCCCTTGTGGCTACTGGAATTAATGATTTGCTGGTTGTTTCAT 2864
 QY 1649 IleSerValSerAlaAlaGlyPheHisLeuGlnTyrLysThrValGlyLeuSerSerCys 1668
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 DB ----- 2906
 QY 1709 MetProGlyThrValAlaArgTrrPheAsnTyrProProProLeuSerCysIleAlaGlnCysGly 1728
 DB -----GAGTGTGC 2915
 QY 1729 GlyThrVal-----GluGluMetGluGlyValIleLeuSerProGlyPheProGly--- 1745
 DB |||||
 DB 2916 GAGCATGTAAGCAAGATTAAGAAACCAAGATCTGACTACATGCTGCTGGTGGAT 2975
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 QY 1821 HisSerGlnAsnArgProGlyPheLysLeuGlnTyrGlnAla 1834
 DB |||||
 DB 3216 GACACATCAACAAAGAGATTTCAATTAAGATTAACAAAGC 3257

RESULT 14

US-08-866-650-4
 Sequence 4, Application US/08866650
 Patent No. 5939321

GENERAL INFORMATION:

APPLICANT: Greenspan, Daniel S
 APPLICANT: Takahara, Kazuhiko
 APPLICANT: Hoffman, Guy G
 TITLE OF INVENTION: Mammalian Tolloid-Like Protein
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Quarles & Brady
 STREET: 1 South Pinckney Street
 CITY: Madison
 STATE: WI
 COUNTRY: US
 ZIP: 53703

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/866,650
 FILING DATE:

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Berson, Bennett J
 REGISTRATION NUMBER: 37094
 REFERENCE/DOCKET NUMBER: 960296, 93839
 TELEPHONE: 608-251-5000
 TELEFAX: 608-251-9166

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
 LENGTH: 3919 base pairs
 TYPE: nucleic acid

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STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 648..3689
OTHER INFORMATION: /product= "human mt11 protein"
US-08-866-650-4

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Alignment Scores:
Pred. No.: 3,896-48 Length: 3919
Score: 768.50 Matches: 245
Percent Similarity: 37.83% Conservative: 131
Best Local Similarity: 24.65% Mismatches: 331
Query Match: 4.52% Indels: 287
DB: Gaps: 33

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US-10-016-248-2 (1-3104) x US-08-866-650-4 (1-3919)

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QY 879 AAsnAhiGluCysIleTySerIleGlnThrGlnProGlyLysGlyIleGlnLeuLys 898
DB 1419 GATACCACTGTAATCATCATAGAGAAACATCCAGCCAGGTCA----- 1463
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DB 1503 TCA-----CTTGAGAAAGATATGATTTGCACAGTATGCACTATGCGCAGGAAC 1553
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DB 1554 ACCCTTCAAGGGGAGATGTTTGGATACCATTTCTCCCTCCCGT----- 1598
QY 958 PheGluLeuHisPheSerSerPheGluLeuLysCysGluAspProGly---ThrPro 976
DB 1599 -----GATGATATGCGCATACGTCCT 1619
QY 977 LysPheGlyTyTyLysValHis---AspGluGlyHisPheAlaGlySerSerValSerPhe 995
DB 1620 GCAATTTGGTCAGGACCCGCTTAAGCAAGAGATATCCACAGCA----- 1667
QY 996 SerCysAspProGlyTyTySerLeuArgGlySerGluGluLeuLeuCysLeuSerGlyGlu 1015
DB 1667 ----- 1667
QY 1016 ArgArgThrTrpAspArgProLeuProThrCysValAlaGluCysGlyGlyThrValArg 1035
DB 1668 -----AGAAAGCTGTATAGATGCCAGCA---TGTGAGAAATCTTCAACA 1709
QY 1036 GlyGluValSerGlyGluValLeuSerProGlyTyTyProAlaProGlyGluHisPheLeuVal 1055
DB 1710 ---GAATCCATAGCACTTCTCTCCAGAGATTTCCCAATGCGTAACTCTTTACACA 1766
QY 1056 AsnCysIleThrThrIleGluAlaGluAlaGlyCysThrIleGlyLeuHisPheLeuVal 1075
DB 1767 CACTGCATCTGGAGAGTTTCTGTGACCCCGGAGAGAAAGATTTGTTAAATTTTACAAAG 1826
QY 1076 PheAspThrGluGluVal-----HisAspValLeuArgIleThrAspGlyPro 1091
DB 1827 ATGATCTATACAAAGAGTAGTTGTGCTGTATGACTATATGAGTAAAGAGACGGGTAC 1886
QY 1092 ValGluSerGlyValLeuLeuLysGluLeuSerGlyProAlaLeuProLysAspLeuHis 1111
DB 1887 TGGAGAAATACACTCTCTCTGTGTAGATTTCTGTGGGACAAATTTGCTGAGTTTACT 1946
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DB 2024 ----- 2024
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Db      3302  ----- 3302
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; Sequence 4, Application US/09021287
; Patent No. 5981717
; GENERAL INFORMATION:
; APPLICANT: Greenspan, Daniel S
; APPLICANT: Takahara, Kazuhiko
; APPLICANT: Hoffman, Guy G
; TITLE OF INVENTION: Mammalian Tolloid-Like Protein
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53703
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/021,287
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/866,650
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Berson, Benet J
; REGISTRATION NUMBER: 37094
; REFERENCE/DOCKET NUMBER: 960296, 93839
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3919 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 648..3689
; OTHER INFORMATION: /product= "human mtII protein"
US-09-021-287-4
Alignment Scores:
Pred. No.: 3,896-48 Length: 3919
Score: 768.50 Matches: 245
Percent Similarity: 37.83% Conservative: 131
Best Local Similarity: 24.65% Mismatch: 331
Query Match: 4.52% Indels: 287
DB: 2 Gaps: 33
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Qy      899  AlaArgAlaPheGluLeuSerGluGlyAspValLeuLysValTyrAspGlyAenAenAsn 918
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Qy      919  SerAlaArgLeuLeuGlyVal-----PheSerHisSerGluMetMetGlyValThrLeuAen 937

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Qy      958 PheGluLeuAlaPheSerSerPheGluLeuIleuLeuSerGlyAspProGly----ThrPro 976
Db      1599 -----GATGATATGGCATACGCTCT 1619
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Qy      996 SerCysAspProGlyTyrSerLeuAlaGlySerGluLeuLeuCysLeuSerGlyGlu 1015
Db      1667 ----- 1667
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Qy      1056 AsnCysIleTrrPheIleGluAlaGluAlaGlyCysThrIleGlyLeuHisPheLeuVal 1075
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Qy      1076 PheAspThrGluGluVal-----HisAspValLeuArgIleTrrPheGlyPro 1091
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Qy      1344 HisGlyGlyTyrGluValGluGlyThrSerThrLeuSerCysIleLeuGlyProAspGly 1363
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Db      2577 TGTGTGTGGCAAGTGTGTGCACCAACCAAGTACAGAAATTTCTGTGAAGTTGATTTT 2636
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GenCore version 5.1.6
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OM protein - protein search, using SW model

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Title: US-10-016-248-2

Perfect score: 16985
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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and is derived by analysis of the total score distribution.

SUMMARIES

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3	1555	9.2	2489	US-09-911-842A-5	Sequence 5, Appli
4	1390.5	8.2	3623	US-09-341-461-2	Sequence 2, Appli
5	1375	8.1	1947	US-09-612-314A-52	Sequence 52, Appli
6	1362	8.0	2039	US-09-612-314A-52	Sequence 52, Appli
7	1362	8.0	2039	US-09-612-314A-52	Sequence 52, Appli
8	1267.5	7.5	1847	US-09-612-314A-52	Sequence 52, Appli
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18	768.5	4.5	1013	US-09-021-287-5	Sequence 5, Appli
19	768.5	4.5	1013	US-09-240-473-5	Sequence 5, Appli
20	768.5	4.5	1013	US-09-285-385C-20	Sequence 20, Appli
21	760.5	4.5	1023	US-10-140-002-200	Sequence 20, App
22	750	4.4	1015	US-09-285-385C-2	Sequence 2, Appli
23	746	4.4	986	US-09-285-385C-19	Sequence 19, Appli
24	744.5	4.4	788	US-08-572-225-1	Sequence 1, Appli
25	738.5	4.3	1013	US-08-866-650-3	Sequence 3, Appli
26	738.5	4.3	1013	US-09-021-287-3	Sequence 3, Appli
27	738.5	4.3	1013	US-09-240-473-3	Sequence 3, Appli

28	703	4.1	910	4	US-10-140-002-112	Sequence 112, App
29	702	4.1	986	3	US-08-872-757-4	Sequence 4, Appli
30	702	4.1	986	4	US-09-850-048A-4	Sequence 4, Appli
31	666.5	3.9	830	1	US-08-110-158-4	Sequence 4, Appli
32	663	3.9	591	3	US-08-991-408-4	Sequence 4, Appli
33	663	3.9	591	3	US-09-432-473-4	Sequence 4, Appli
34	648.5	3.8	830	5	PCT-US91-05059-2	Sequence 2, Appli
35	630	3.7	830	6	US-09-475-460A-32	Sequence 32, Appli
36	609.5	3.6	574	6	US-08-365-470-3	Sequence 3, Appli
37	528	3.1	610	1	US-09-209-668-19	Sequence 19, Appli
38	528	3.1	610	3	US-09-009-490A-89	Sequence 89, Appli
39	526	3.1	610	6	US-09-475-460A-32	Sequence 32, Appli
40	502	3.0	611	4	US-09-748-061A-32	Sequence 32, Appli
41	502	3.0	611	4	US-08-435-149-3	Sequence 3, Appli
42	501	2.9	577	2	US-08-872-757-2	Sequence 2, Appli
43	501	2.9	730	3	US-09-850-048A-2	Sequence 2, Appli
44	485	2.9	730	3	US-09-850-048A-2	Sequence 2, Appli
45	485	2.9	730	4	US-09-850-048A-2	Sequence 2, Appli

ALIGNMENTS

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RESULT 1
US-09-911-842A-4
; Sequence 4, Application US/09911842A
; Patent No. 6656707
; GENERAL INFORMATION:
; APPLICANT: Amgen Inc.
; TITLE OF INVENTION: C3B/C4B COMPLEMENT RECEPTOR-LIKE MOLECULES AND USES THEREOF
; FILE REFERENCE: 01017/37592
; CURRENT APPLICATION NUMBER: US/09/911,842A
; PRIOR FILING DATE: 2004-07-24
; PRIOR APPLICATION NUMBER: US 60/222,438
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 3594
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1757)..()
; OTHER INFORMATION: Xaa = any or unknown amino acid
US-09-911-842A-4
Query Match 10.9%; Score 1850.5; DB 4; Length 3594;
Best Local Similarity 21.3%; Pred. No. 8.4e-134;
Matches 789; Conservative 378; Mismatches 1170; Indels 1369; Gaps 149;
99 TCNEGYDLGGSKRTCTMKVSDMFAWSDHRCVCRARCDALHRCGRTSPNFPIDYN 158
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540 -----DS-----CGKQPA 547
219 TPG-----SRIP-----SMGDIWROKTV-----LEICRDISSDARSVRS 259
548 RPKMTQLSGRGVYLSGVAVCATSG-----KMSAKVGTAVCKDV-----EA 591
260 PRTSNVAVLAPGTETIEQSGCGDPGIPAYRRGSRPHHCDTLKFCQPAFE-----LVG 314
592 PQLSCPDIDAKTGEOODSANATWQVPT-----AKNSGEKVSVHVPAFTPTPYLPFG 645
315 QKAITCQKNQWNAKKRGCVFS-----CFRNTSPSGV-VLSPNYEDYGN 360
646 DVAITTYATVS-GGNQASCTFYIKVIDEPPVIDWC-----RSPPIQVKEKHPASWD-- 698
361 LHCWMLIAPRESRIHLAFNDIDVEPOFDELVIKDGATAPVLTGFS-GNQLPSSITSS 419
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Db 699 -----EPQF-----SDNSGAEIWLTSHTQDMFPHGTVV 729
 QY 420 GHVAREFQTDHSGKRGFNITFTFRHNCBPDGAVNGKRKRDSDLSQLGSSISFUCDEG 479
 Db 730 WYRA-----IDPSGNNTTCOI-HIVIKSPCEVPFTVNGDFICADDSAGVNCSLCKEG 783
 QY 480 FLGTQGS-ETITCVLKEG-----SVVNSAVLRCEAPCG-----G 513
 Db 784 YDFTEGSEKYYCAFEDEGIWRPYPSTWPCAIKRFANHGFKSFEMLYKTRCRDDMDLFX 843
 QY 514 HLTPSSTIISPCMPGYKXA-----LSCAMVTEAOPGP-----I 549
 Db 844 KFAFAEFTIGANNVPSPCNADADDICRLBDLTKKYCIENVYNYENGFAIGCGWGANRL 903
 QY 550 KITFDREKTEVNYDLEVRDGR-----TYSAPILGVYHGT---Q 565
 Db 904 DYSDHDLVYQETFPDVGAKSSRIKRYPLSDPKIQLIFNITASVPLPEEKNDLTLE 963
 QY 586 VPQFLIST-----SNLYLFTSDKSHSDIGFOLRYETITLQSDHC-----LDGIPV 633
 Db 964 NQORLITLLETITNRLKSTLNKEPMYS---FOLASETVADSNLSLEKAFLECRGSLV 1020
 QY 634 NGOR-----HGNDPYGALVTFSCDSGYTLSDGEPLCE-----PNFQMSALPSCBA 681
 Db 1021 RGRMCVNCPLGTSTYSLEHSTCESQLMGSYODEGQLECKLCPPRTHAELYHLSHVSSECKA 1080
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 Db 1081 QCGQGTSSSGLETCEBPLGTYQPERGSRCLCEPTEITTVKRAVIDISACGVPCEVB 1140
 QY 695 -----LSGFRP---DEYPNN-----LNCTW-----711
 Db 1141 FSRSGLTCPYCPRDYQPNAGKSFCLACPFYGTITITGATITGDSFSSTPSAEBES 1200
 QY 712 --IIISHGKGVF---FTPTTHL-----ESGDYLLITENGSETPQLRLQTLG- 754
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 QY 828 YRLEGRA-----RITCLGRRRLMSSPLPRVACGNSVGTGOTGLSPNPNVY 877
 Db 1366 TRCEKXVDECLSQPCQNGATCKDGANF-----RC-QCPAGFTGTHCEL-----NI 1410
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 QY 925 VBSHSEMGV---TLNSTSSLMV---DFTT-----DAENT-----SKGPELLRS 963
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 QY 979 ---GYVHDEGHA-----GSSVSPSCDPGYSLRSEELLCTIS 1013
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 QY 1014 GERRTVDRPLTPCV-AEGG---GYVAGEVSGVLSGYPAPYEHNNLNCWTIEAAGCTI 1069
 Db 1701 --QGGWTOGFLPHCERIRCGLPALENGFSABDFHAGSTVYQ-----CTS 1744

QY 1070 GLHFLVPTDEBVHDLVLRINDGPVESGVLLKELS-----1102
 Db 1745 G-YLLIGDSRMFCXDNGSWNGISPSCLDVBECVAGSDCEHASCLNTNGSYVCSNPNPYT 1803
 QY 1103 -----GPALPKDLHSTFNSVVLQFSTDFTSKOGFALIOFS-----VST 1140
 Db 1804 GGGKXCAEPVKKCAENPENGRS-----SGELYT--VGTAVYFSCDEBHELAVGT 1852
 QY 1141 AT-----SCNDPGI PONGSRSGDSWEAGDSTVFOCDPGVALQSGAETS 1183
 Db 1853 ITCLETEGWDRLRPCECAISCGVPVPENGVDGSAFTYGSKYVYRCDKGYTLISGDEESA 1912
 QY 1184 CVKINERFMQSPPTC-IAPCGDLTGSVYILSPNPERPPEKCECMKTVBPDYI 1242
 Db 1913 CLASGS---WSHSSPVCGLVC-----SQEDINNCK-----YTL 1944
 QY 1243 A-----LVFNIFNIEBPGYDFLHIYDGRDLSPLIGSFYGSQULPGRITSSNSLFLAFRSDA 1298
 Db 1945 SGLTYTLSTIASYSCENGYSL-----QGSLLLECTASGSW-----DR 1979
 QY 1299 SVSNAGFYIDYTENPRESCPDGSIKNGTRVGSDLKLSVYTYHGGYEVEGTSLCT 1358
 Db 1980 APPSCOLV-----SCGEPPIVKDAVITGNSNFTFGNTVAVYCKEGYTLAGPPTIIC- 2029
 QY 1359 LGPDGKPVNNRPVCTAPCGGQYVSDGVLSPNYPONITSGQICLYFVTVPKD-YVVF 1417
 Db 2030 -QANGK--MNSNHOCLA-----VSCDEPVPVDHAS-----PETAHRLF 2065
 QY 1418 GQFAFFHALNDVVEVHDGSHQSHRLSLSGSHTESLPLATSNQVLIKFSAKGLAAPPAR 1477
 Db 2066 GDTAFYYCA-----DQYS-----LADNSQLCNAGMNVPPRG 2098
 QY 1478 GRHFYVQVPRTSATQSGSVPEPRYG---KALGSPFSICALYRFGCSGYALQSPBEIJC 1534
 Db 2099 ---QAVPRCIAFCEKPEPSVSYLSIESVSKAKFAAGSVVSPFCMGEGFVLNTSAKIEC 2152
 QY 1535 LFPVGAQOMNVNAPVCTVPCGQNLTERGTLISGPFEPYUNSLNCWKIVVPEGAGIQ 1594
 Db 2153 LR-----GGENS-----PSPL-SVQC-----2167
 QY 1595 IQVVSFTEQWDSLEVEDGADNTVTLMSFSGTVPALLNSTSNQVLIHFYSDISVSA 1654
 Db 2168 -----IPV-----2170
 QY 1655 GEHLEYKTVGLSSCEPRAVPNGVKTGERLYLVNDVYSQCEBRYALQGHANISCMPIYR 1714
 Db 2171 -----RCGEPPSIANGYPSGTNYSFGAVVAVYCHKGFYIKKKSTC--EATG 2216
 QY 1715 RWNYPPLICIAQCGGTVEEMEGVILSPGFPCNYPSPNMOCSWKIALPVGFAHIQFLNFT 1774
 Db 2217 QMSKPTPTC-----HP--VSCNRPKVENGFLEHTTGRTES 2251
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 Db 2252 EARFOC---NPGYKA-----AGS-PVFPVQANR---HMSDAPLSTCPL-----2288
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 Db 2289 ---NGKRPPIQGFLEGSFEVGSKVQFVCNBEYELVGNWSWTCQ--KSGKSKKSP 2342
 QY 1894 KCEVP---CGGNITSNGIVYSPGFPSPYSSQDCWMLITVYIGHVRLNLILQTEPSG 1951
 Db 2343 KC-VPTKCAEPPLLENQVLKE-----LABEVGMTISCEGHALO-GPSVLKCLB9GQ 2394
 QY 1952 FITTWDEPQOQTAPRLGVFTRSMAKTVOSSNQVLLKFRDAATGGLFALAFSAVPLTK- 2010
 Db 2395 ---WNG-----SFPICKM 2404
 QY 2011 ---CPPTILPNAFVTENEFNIGDIYRCLBPFTLVAGNEILCKLGTIYQFSGPPIC 2068
 Db 2405 VLCPSPPLIPRG-VPASSGALHFGSTVTKYLCVDGFFLRGSPITLCOADS--TWSSPLPEC 2461

QY	2069	ENHCPTNELLTDSNGVILSOSYPESYQFOFCMSLVAVEBDYNISLVEFYLBKQVDE	2127
Db	2462	VPECEPOEEELN-GIITHVGLAVLSTTLTYC-----KGFEL-----VGN	2501
QY	2128	FEIFDPGSGO-----SPLIKALSGNYSABLIVTSSNSVYLWSSDHAYNRKGFIRYSAF	2183
Db	2502	ATTLGEGNQWLGKPMCKPIE-----	2523
QY	2184	YCSLEPRADLHGFILGOTSTORPGSIHFQCNAGYLVGHSMALCTRHPOGYHLSBALPLC	2243
Db	2524	-CPREKEILNG-OESSVSFOYQOITTYCDRGFRLEBGRKSLTCLCTED----KMDMPSC	2577
QY	2244	QALSCGLEAPRNKGNVPKEKEYTGVTKAYVCSSEGHLOAGAEATPACLDCTLMSNRNVP	2303
Db	2578	DAIHOSDPOPIENGVEGADRYGKMIIITVSCPGFQVLGHMQT--CEBSG-WSSSS--P	2632
QY	2304	QCVPTVC---PDV---SSISVEHGRWRLIFE-----	2338
Db	2633	TCVPIDCLPHHIDRCDCCTKXRDQGNHDOEDDMVEVYLAHPHLETAALNTYESP	2692
QY	2329	---TOYFOAOLMLICDPGYTYTGQVIRICQANGKWSLGDSTPTCRILISGELPI-PPN	2383
Db	2693	ASHASHFLYGTWVSVCSEPGYELGIPVLICQEDQTN--GTASCSISIEC-DLPVAPEN	2749
QY	2384	GHRIGTSLVYGATALFSCNSGTYLVGSVYRECMANGLMSGEVNLACHGCTPEPIYNGH	2443
Db	2750	GFLHPTOTJMSAQAQYSCKPGHILIEGSHRLCLQNKQMSGVTPRCEALISCKKPNPLWNGS	2809
QY	2444	INGERYSYRGSVYVQCNCNAGFRLIGMSVVICODDHMSKTPFCVPITGCHGNVNGLTQ	2503
Db	2810	IKGDDYSILGVLYHECDSGYILNSKKRTCCQENRDMDHCMICPIVDGSGSPVPTNGRYK	2869
QY	2504	GNQFLNDVYKFCVNCPIGYMAEGAARSOCLASGOWSDMLPTCRINICTDPGHQENSVRQVH	2563
Db	2870	GGEYTFQKEIITYSCHEGFLIEGANSRICLTJNGMSGATPCMCAPRCAPQVPRNGV----	2925
QY	2584	ASGPRRSEFGTIVSYRCHNGFYLLGTPVLSQCGDGTWRRPAPQCLVNSCGHPGSPHSQM	2623
Db	2926	ADGID-YGFKKEVAHACLEGVYLQCAPRLTCCOSNTMAEVPVCKPAPCCGPRADLPQGF	2984
QY	2624	SGDSYTVAVVYRSGTICRKLTVGNSYTBWCGLDGHNYSLPHC-----SGT	2668
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QY	2669	SVGV-----CGP-PGIPAHGIRLGSF	2689
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QY	2690	DPGYMYRSCAGHVLKGSSEPTCOANGMSGSGOPECGVISCGNPATPSNA-----	2740
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QY	2741	-----RVVF-SDGLVFS	2751
Db	3164	ESKYKLRLEGVYMSDSDTDTFTCOQDGHVBERITCSBKCKPVBNSMTRIRIFHDDDPQVN	3223
QY	2752	SSIIVECREGYATGILSRHCSVNGTWTG--SDEPCLVINGCDGCIIPANGRLANGDPRYN	2809
Db	3224	ROYVSCAEGTTHEBVNMSTQCPDQTPWPPSPDSDECIYVUCGHESPRAHSGVGNKXISFG	3283
QY	2810	KTVVYQCVGYVMESHVSVLSCTKDRTWNGTKPVCKALMKCPPLPIPNGRVYSGDFWVG	2869
Db	3284	STIVYQCDPGYKLEGNRERI--CQENRQMSGEVAVACRENRCETAPFNGKAVULENTTSG	3341
QY	2870	SSVUYACLEGGQLSLPAVFTCEGNSWTGELPQCCPVPVCGPQV-PSNGRREDGFSYRS	2928
Db	3342	PSLLEPSSCHRGYTLBESPRAHCTANGTWNHLTPCLKPNCBPAPVPIPENAVULSEKEXFYVDQ	3401
QY	2929	SVSFSCHPPLVYVGSPPRFCSQSDGWSGTQSPCIDPLTTLTADGCVPOFGIQQNNSOG--Y	2986
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QY	2987	QVGSVLEFRCKGKYLLOGSTRITCLPNLTWSGTPEDCVPHHCRQETPHANVAGALDLP	3046

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Db      3456 QYGDMMITYSCISGTMLEBSLRSVLENGTW-TTSPVCRACVCRFP-----CONGGVCCQRN 3509
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Db      3510 ACSCEPDGMMGRRLC-----EETICILPLCINGRCVAPQCCDCPTGM 3549

RESULT 2
US-09-911-842A-2
; Sequence 2, Application US/03911842A
; Patent No. 6656707
; GENERAL INFORMATION:
; APPLICANT: Amgen Inc.
; TITLE OF INVENTION: C3B/C4B COMPLEMENT RECEPTOR-LIKE MOLECULES AND USES THEREOF
; FILE REFERENCE: 01017/37592
; CURRENT APPLICATION NUMBER: US/09/911, 842A
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: US 60/222,438
; PRIOR FILING DATE: 2000-08-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 3571
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-911-842A-2

Query Match      10.6%; Score 1794; DB 4; Length 3571;
Beet Local Similarity 21.3%; Pred. No. 2,1e-129; Indels 1354; Gaps 155;
Matches 799; Conservative 393; Mismatches 1211;

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QY      130 VCRARMCDAHRGGS-GITTSNPPIQYDNNACVMTITALNBSKVITKLAFFEEFDLERGY 188
Db      432 YCRVRTC-PIRLQRPQGHISCTSTEMLYKTT--CL-----VACDEGYRLEGS 475
QY      189 DTLTV-GPGGDDGPGOKTVLYMSQACSD-----SPHTPG----- 221
Db      476 DKLTCQGSQWDGPEPRCV--EHNCSFTQMPKDIITSPHNCGQPAKFGITCYVSCRQG 532
QY      222 ---SRIPESM---SGDIWRQKMTV---LEICRDISSDARSAGSVKSPXTSNABELVAP 271
Db      533 FILSGVEMELACTISG-----KMWVGQAQAVCKV-----EAPQINCPKDI EAK 576
QY      272 GTEIEQSGSCDGGIIPAYGRREGSRFHHDITLKFEQCPAFE-----LVQKALITCQKNQW 326
Db      577 TLEQODSANVTWQIPT-----AKDNGGEKVSVMHDAFETPPYLPVGDVAIVTYATD-L 629
QY      327 SAKRPGCVCSFNFPTSPSGVULSPNYPEDYGNHLHCWMLLARPERIHIAFPDIVER 366
Db      630 SGNQASCTFHLKVIDAEPPVIDMCRSEPP-----VQVSEKVAHAWD--EP 673
QY      387 QFDELVIKDGATAEAPVLTGFS--GNQPSITSSGHAARLEFOTDHSCTGKRGFVITFTTF 445
Db      674 QF-----SDNSGALVITRSHITQDLPFGSETIYQYTA-----TDBGNRRITCDI-HIVI 722
QY      446 RHNECPDPPGVVNGKRFEDSLQGLSSISFLCDEGFLQTQGS-ETITCVLKEGVSVMNSAV 504
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QY      505 LRCAAPCGGHLTSSSG-----TILSPGMPGFYKDA--- 534
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QY      535 -----LSCAMVLEAQGPV-----IKITFDRKTEVNTDLEVRGR- 571
Db      841 DCRLEENLTKKYCLEVYIDYENGAIEPGCGKAANRLDYSDYDFLDIVQETATISIGNAKS 900
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Db 901 SRIKSAFLSDYKIKLIFENITASVPLPERNDTLEMENQORLLDTLETITKLTAKTANKD 960
 Qy 605 KSHSDIGQLRYETI-----TLQSDHCLDPSI PVNGORHGN-----DFYVALVTFSQ 652
 Db 961 PMYS---FQLASELLIDNSNLETKKASPCRPFSVLRGMCVNCPLGTY--NLBHFCT 1015
 Qy 653 DS-----GYLSDGEPLCE-----PWFQSRALPCEALCG-----684
 Db 1016 ESHCIGSYQDEEGC-LECKLCPGMYTEYIHSRNISDCKAQCKQGYVSYLETCESCL 1074
 Qy 685 GFIO---GSGCTILSP-----GFP-----DFYNN 706
 Db 1075 GTYQPKFGSRCLSCPESTSTVKRGAVNISACVPCPEGRSGMLPCHPCRDYQPN 1134
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 Qy 761 ISAG-----LYGNFTAQV---RFISDFMSYSGFNITFSEYDLR 797
 Db 1178 ASLGHIKRHEISSQVHECFENPCNHSCTCOQLRGYVCLCPGLGTGLK---CETDIDE 1234
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 Db 1235 CS---PLPCLMNGVCHDLVGEFICEPSCGYTGRCENINECSSPLCKKGI CVDGVAG 1290
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 Db 1411 PGFSGKRCETEOSTGFNLD---FEVSGIYGYVMDGMLPSLHALTCTFMWKSDDMNYGT 1467
 Qy 906 -----EGDYL-----KYY 913
 Db 1468 PISYAVDNGSDNLTLLDYNQWLVYVNGREKINCPADVADRWHHAIITWTSANGIKWY 1527
 Qy 914 -----DGN-----NNSARLLGV-----FHSHEMMGVTLINSTS-SLWLDPI 948
 Db 1528 IDKLSDBGAGLAVGVLPIPGGALVVGQEQDKKGEFSPAESF---VGSIQNLNM-DYV 1583
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 Qy 1041 QVLSPEYRPAEYENLNCIWTIEAAGCTTGL-----HVLVPTBEVHDVLRITWGPVBSG 1095
 Db 1686 ERISCCVPPLENGFHS--ADDFYAGSTVYOCNNGYILLGDSRMFCTDNGSMNGVSPSC 1743
 Qy 1096 VLLKELS-----GPALPKDLHSTFN 1115
 Db 1744 LDVDECAVSGDCSEHASCLANDGSIYCSVPPYTDGKCAEPICKAKAPGPNENGHS-G 1802
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 Db 1803 ELYTVGAETVFSQOEBEYQLMGVTKITLESSEMNLIPYKAVASGKPAIPENGCIEBLA 1862
 Qy 1160 WEAGDSTVQCPDGYALOGSASIECYKIKENRFQWQSPPTCLAPCGGLITGSSVILSPN 1219
 Db 1863 FTFGSAVYTRCKNGKGTLLADGKSSCLANS---WSHSPVC-----1900
 Qy 1220 YBEPYPGKEDMWKTVTSPDYIALVFENLEPGVDFLHYDGRDSTPLIGSF---YG 1276

Db 1901 --EPV-----KCS-----SPE-----NINNG--KYILSLGLTYLSTASYCDTQYS 1936
 Qy 1277 SOLPRIESSNSNLFIAFASDASVSNAGFVIDYETENPRESFCDPQSGIKKGTGRGSDTLKG 1336
 Db 1937 LQPSIIECTAGSIW-----DAPRACHLV-----CCEPAIKAVITGNPFR 1982
 Qy 1337 SSYTYCHGGEVEGTSTLSCILGPDGKPVNNPVPCTAPCGGQYVSGDGVLSNPYQ 1396
 Db 1983 NTVYTYCKEYTLAGLDTIECL--ADGK--WGRSDQOCLIA-----VSCDEBP 2025
 Qy 1397 --NYTSGOICLVFVVPKDYVFGQFAPFHTLNVVEVHDGSHQSRLLSSLSGHTBE 1454
 Db 2026 IVDHASPEHA-----HRLFGDIAFYCS-----DGYT-----2052
 Qy 1455 SLPLATSNQVLIKFSAGKLAAPRGHFVYQAVPRTSATQSSVPEPRYV---KRLGSDPS 1511
 Db 2053 ---LADNSQLLCNAQKQWVPEG-----QDMPRCIAHCEKRPVSIVLSBSKAKA 2103
 Qy 1512 VGAIVRFEGNSGYALQSPETIECLEVPGALADNNVSAFTCVVPCGGLTERGTTLSPGF 1571
 Db 2104 AGSVVSFKMBGFLVINTSAKIECM---RQGMN-----2133
 Qy 1572 PEPYLNISNCWKIIVPBGAGIQIVASFVTEQUNDLSEVFDGADNTVTLGSPSGTTP 1631
 Db 2134 PSPM--SIQC-----IP 2143
 Qy 1632 FQCEPVALOGHAHISCMPTVRNMYPRPLCIAQCGTVEMBEVILSPGPGYPSNM 1751
 Db 2170 VSCNKGPIYIKBKSTC--EATQWSSPIPTC-----2199
 Qy 1752 DCSWKIALPVGGAHIOFLNFTSEPNHDYIEIRNGPYETSRMMGRFSGSELPSLSTSH 1811
 Db 2200 ---HPVSCG-----BPP---KYENGFLE-----H 2217
 Qy 1812 ETTYVPHSD-HSNRPGK-LEYQAYELQ-----ECDDPEPPANGIYRG 1853
 Db 2218 TTRGFEESEVRVYQCPGYKSVSGFVQCANRHHMSEPLMCPVLDCKPPIQNGFMKG 2277
 Qy 1854 AGYVNGQSVTECELPYQVLTGHPVLTGHNRMMDHPL-PKC-----EYPCGN-----1902
 Db 2278 ENFEVGSVNGFPCNBGTYLVDSSWTCQ--KSGMKNSNPKCMAPKCEPPLLENQVL 2335
 Qy 1903 --ITSSNGTVYSPGPEPSSSQDCWMLTVPIGHGVLNLSLLQTEBSGDFITWGPQ 1960
 Db 2336 KELTTEVGVV---TFSCKE-----GH-VLOGPSVLKCLPSQO---MN---2370
 Qy 1961 QTAPRLGVFTSRMAKTVQSSNQVLLKFHNDATGGIFALAFSAIPLTK---CPPTIL 2017
 Db 2371 -----DSPVCKVILCTPPELI 2387
 Qy 2018 PNAEVTENEENFNGIDIVRYRCLPFTLVGNEILTCKL-GTYLOFESPPPIC-EVHCPTN 2075
 Db 2388 -SFGVPIPSALHFGSVYKXSCVGGFRLRGNTLLQCPDGTW---SSPLPECVVEBPQ 2443
 Qy 2076 ELLTDSGTVILSQYPSQYFQTCMSLVXVEPDYINISLVEYFLSEKQYDEFEI FDGPS 2135
 Db 2444 EETPN--GLIDVOQLAVLSTALTYC-----KPGFEL-----V 2473
 Qy 2136 GQSPPLKALSGNYAPLITVSSNSVYLRFWSSDHAVNRKGFKIRYSAFYQSLPAPLHGF 2195
 Db 2474 GNTTTLGGENGHW-----LOGKPLCAKIECLKREILING- 2507
 Qy 2196 ILGQTSIQPGSIIHFGCNAGYRLVGHSMALCTRHPOQYHLMSEAIPLCOALSGCLPEAPX 2255
 Db 2508 KFSYTDLHYQVYVYSCNRGFRLEGPALTCLETGD---WDVADAPCNMHIHDSPPRIE 2563
 Qy 2256 NGWVFGKXYVTKKAVYSCSEGYHLQAGATATBCLDTGMSRNNVPQCVPTC-----2310
 Db 2564 NGFVEGADYSYGAIIITYSCPPGF--QVAGHAMQTEBSG-WSSS--IPTCMPIDCGLBPH 2618

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Qy 2311 ---PDVSIIVH-----RWLIFE-----TOYQO 2334
      |:::|:::|
Db 2619 IDGDCCKLADDOCFEEOEDDMEEVYTPHPHLCALVAKTMENTESPATHTSSNPLYG 2678
      |:::|:::|
Qy 2335 AOLMLICDPGYTYYTGAVIRCOANGKWSLSDPTCRILISGELPIPNGRIGTLISVG 2394
      |:::|:::|
Db 2679 TWSYTCNPGYELLGNPVLICQEDGTWN--GSAPSCISIEDDLTAENGLARTETSMG 2736
      |:::|:::|
Qy 2395 ATAFSCNSGYTLVGSRAVRECMANGLWSGEVRLACHCTPEIYVNGHNGENYSTVGS 2454
      |:::|:::|
Db 2737 SAVOYSCPGHILVGSDLRLCLENRKWSGASPRCEAISCKKPNVNMNGISIGSVYLYST 2796
      |:::|:::|
Qy 2455 VVYOCNAGPRLIGSVIRICODDHMSGKTPCEVPIITGCHGNPNVNGITOGNOFLANVVK 2514
      |:::|:::|
Db 2797 LYIECDGIVLVNGERTTCODDKMDEDEFLCIPVDCSSPRVANSNGVGRGDEYTPQKEIE 2856
      |:::|:::|
Qy 2515 FVCPNPGYMAEGAARSQCLASGOWSDMLPTCRILINCTDPGHQENSVRQVHAGPHRFSFGT 2574
      |:::|:::|
Db 2857 YTCNEGFLLEGARSVCLANGSWSGATPDCVPRVCAPIPOLANGVTE-----GLDYGFPMK 2911
      |:::|:::|
Qy 2575 TVSYRCHGFIYLGTPVLSGCGDGTWRPRPQCLVSCGHPGSPHSQMGSDYTVGAVV 2634
      |:::|:::|
Db 2912 EVTFHCHGFIYLGAPLITCQSDGNMDAELPLCKPVNCGPREDLAHGFPMGFSEIHGHI 2971
      |:::|:::|
Qy 2635 YSCIGKRTLVGNSTRMC----- 2652
      |:::|:::|
Db 2972 QYOCFPGYKLGHSNRKCLNSGWSGSSPSCLPKRCSTPIVETVNGTDFDCKAARIQ 3031
      |:::|:::|
Qy 2653 -----GL-----DGHWTGSLPHCSGTSVGVCD-PCIPAHGIRLSDPDPGTVMR 2696
      |:::|:::|
Db 3032 CFKGFPLGLSEITCEADGQMSGFPHCHTS---CGLPMIPAFISSTSMWE-NVIT 3087
      |:::|:::|
Qy 2697 FSCGAGVNLGSSGERTCOANGSWSGSQPECGVISCNPGRTPSNA----- 2740
      |:::|:::|
Db 3088 YSCRSYVIOGSSDLICTEKGVWSQPYVCEPLSCGSPSVANAVATGEATYESVYKLR 3147
      |:::|:::|
Qy 2741 ----- 2758
      |:::|:::|
Db 3148 CLEGYTMDTDTDTCTCKCKGRMPERJISCEPKKPLPENITHILVHGDDPSVNRQVSVSC 3207
      |:::|:::|
Qy 2759 REGYVATGLSRHCSVNGTWTG--SDPECLVINGCDPGIPANGHLANDFRYNKTVTYQC 2816
      |:::|:::|
Db 3208 AEGTTFEGVNIISVQDLGTWEPFRSDSCFVSCKGESPHEHGVSGKTFESTIITYQC 3267
      |:::|:::|
Qy 2817 VPGVMESHRVSVISCTKRTWNGTKPVCAKLMCKPPLIPNGKVSGSDFMSSSVTYAC 2876
      |:::|:::|
Db 3268 EPGYELEGNREVR--COENRQWSSGVVAICKETRCETLEFLNGKADIENRTTGPNVYVSC 3325
      |:::|:::|
Qy 2877 LECYQSLPVPFCEGSGWTGELPOCFPVPCDPRV-PSRGRREDGFGYRSVSFSCH 2935
      |:::|:::|
Db 3326 NRGSLSGPSEBAHTEGNTWHPVLPCKPNCPPVPIPENALISEEYVDONVSTICKR 3385
      |:::|:::|
Qy 2936 PPLVIVSPRRFCQSDGTWSTGTPSCIDPILITGADGVPOFGIIONNSQGVYSTVLFR 2995
      |:::|:::|
Db 3386 EGFLOGHGIIITCNPDWTQTSKAC---EKISGCPRAHVENALARGVH-YQYDMITYS 3441
      |:::|:::|
Qy 2996 CQKGYLLQGSTTRCTCLPNLWSTGTPDCVPHHCQPEPTPHANYGALDLS-----M 3047
      |:::|:::|
Db 3442 CYSGYMLEGFLRSVCLNGTWT--SPPIC-RAVCRFP---CQNGICQRPVACSCPEGM 3495
      |:::|:::|
Qy 3048 GYTLITPARASPERVAPSTAPARMAAQAQSRPSAM 3084
      |:::|:::|
Db 3496 GRUC-----EPPICILPCLANGCAVAPYQDCPPGM 3526
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; FILE REFERENCE: 01017/37592
; CURRENT APPLICATION NUMBER: US/09/911,842A
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: US 60/222,438
; PRIOR FILING DATE: 2000-08-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 2489
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-911-842A-5

Query Match          9.2%; Score 1555; DB 4; Length 2489;
Best Local Similarity 20.9%; Pred. No. 4.9e-111; Indels 1224; Gaps 142;
Matches 679; Conservative 332; Mismatches 1021;

Qy 58 KTSVLTVQVGSQGHNNCPDGPGEIPERK-RIGSDPRLGSSVQVTCNEGYDLOGSKRITCMK 116
      |:::|:::|
Db 88 KNSVMTGAKDRCKRKSGRNPPDPVNGMVHVIKGIQSGQIKYSCTGRLIGSSSATCI- 146
      |:::|:::|
Qy 117 VSMFPAASDHRPVCCARMCDALRGPSGIITSPNFPLOYDNNACVMIIT-ALNPSKVI 175
      |:::|:::|
Db 147 ISGDTVIMNETPICDRIIPC-----GLPPIITGDFISTNRENFHGSVVTYRCNPGSGG 201
      |:::|:::|
Qy 176 KLAFFERDLERYDVTLVGDDGQDQKTVLVMSQNAACSHPHTPSRIPEMSGDIWRQ 235
      |:::|:::|
Db 202 RKYFE-----LVGEPS-----YCTSN-----DDOYG-IW-- 225
      |:::|:::|
Qy 236 KMTVLICRDISSDARSQSVKSPKTSNAVELVABTEIEQSGCDP---GIPAYGR 291
      |:::|:::|
Db 226 -----SGRAPQCIIP-----KCTPPNVENGILVSDNR 253
      |:::|:::|
Qy 292 EGRFPHHGDLTKECQPAFLVQKAITCQKNQMSAKKGCYFSCFPNFTSGSVLSP 351
      |:::|:::|
Db 254 --SLFSLNEVEBERCOFGFVMPKPRRYKCOALKMKEBELPSCSRVC---QPPDVILHAE 307
      |:::|:::|
Qy 352 NYPEDGNHLCWMLIARPESRIHLAFNDIDVEPODPFVIDGATAEAPVLGTSGNQ 411
      |:::|:::|
Db 308 RTGRDKNF-----SFGQEVFYS-----CEPGD---LNGAASMRCTPGQDWS-- 347
      |:::|:::|
Qy 412 LPESITSSGHVAREFOTDSTKRGFNITFTFRHNECPD-DGVNNGK-RFGDSIOLG 469
      |:::|:::|
Db 348 -PAA-----PCVYKSCDDFMGQLNGSLVLPVNLQLG 379
      |:::|:::|
Qy 470 SSISPLCDEGFLTQSGSETITCVLKGSVVWNSAVLRCEAPCGHLTSPSGTLLSPGWP 529
      |:::|:::|
Db 380 AKYDFVCDEGF-OLKSSASVYCVLAGMESLIMNSVPCVCE---QIFCPSPVPIPNG--- 430
      |:::|:::|
Qy 530 FYEDALSCAMVIAQGYPIKIFDRFKTEVND-----TLEVR 568
      |:::|:::|
Db 431 -----RHTGKPLEVF--PRGKAVNTCDPHDRGTSGFDLIGESTRICTSDPQ 475
      |:::|:::|
Qy 569 DGRYTS--APLIGVYHGTVQPOPLISTSNLYLLFTGDKSHD--IGFQURVE----- 617
      |:::|:::|
Db 476 GNGVMSAPARCCILIGHCAP-----DHLFPAKLTQTNASFPICSTLSIKYCRPEYVG 529
      |:::|:::|
Qy 618 ---TTLQSDHCLD-----GPIVNGRQG-NDPYGALVTFSCDSG 655
      |:::|:::|
Db 530 RPSPIIT-----CLDNVWSSPKDVCKRKSCTPPDPVNGMVHITDIQVGSRIINYSCTTG 584
      |:::|:::|
Qy 656 YTLSDPELECEN---FQMSRALPCEAL--CGGFIQSSGTTLSGFPFPFYNNNLCTW 711
      |:::|:::|
Db 585 HRLIGHSSAACILISGNAHWSYTPICQRIIPC----- 617
      |:::|:::|
Qy 712 ILETSHGKGVFTFHTFHLESCHDYLLITENGSTFQPLRLQLTGSRRLPAPISAGLYGNFTA 771
      |:::|:::|
Db 618 -----LPTIANG----- 625
      |:::|:::|
Qy 772 QVRFISDF-SMSYEGFNITSEYDLBCEPEVPAYSIKKGLOFGVGDITLTFSCFPG--- 827
      |:::|:::|
Db 626 -----DFISTNRENFH-----YGSVVTYRCNPGSGG 651
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RESULT 3
US-09-911-842A-5
; Sequence 5, Application US/09911842A
; Patent No. 6656707
; GENERAL INFORMATION:
; APPLICANT: Amgen Inc.
; TITLE OF INVENTION: C3B/C4B COMPLEMENT RECEPTOR-LIKE MOLECULES AND USES THEREOF

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QY 828 ---YRLBGTARITCLGRRR--LWSSPLRCAECGNSVTGTGTLSPN--PPVNNNN 880
 Db 652 RKVELVGBERITCTSDNDQVIMSGAPCIT-----PCKCTPBNENG 696
 QY 881 HECTIYSIQTOPGKGIQLKARAFELSEGVDLKVYDGNNSARLLGVPESHSEMMGVTLNSTS 940
 Db 697 -----LIVSDNRS-----LFSLNEV----- 711
 QY 941 SSLWLDFTIDAMENTSKEPELHFSFELKCEDPOTPPKFGYKADHDEGHFASSVSFSCDPG 1000
 Db 712 -----VEFRQCPG 719
 QY 1001 YSLNGSEELLCSGERRTWRPLPTCYAECGTVRGESQVLSPPGAPAYENHNLNCIWT 1060
 Db 720 FVMKGPBRVVKOALNK--WEPELPSCSRVC-----QPP----- 751
 QY 1061 IEBAAGCTTGLHFLVFTBEVHDVLRIMWGVESVLLKELSGPALPKDLHSTFNSVVLQ 1120
 Db 752 -----DVLH----- 755
 QY 1121 FSTDFTSKQGFALQFSVSTATSCNDPGIPQNSRSGDSWEAGDSTVFOCDPGYALQSGA 1180
 Db 756 -----AERTQRDXNFSPOGEVFPYSCPEYDLRGAA 786
 QY 1181 EISCVKIENRFPWQSPPTCIAPCGDITGP--SGVILSPNYPEPYPPGKCDMKVTVP 1238
 Db 787 SMCTPGQD--WSPAFTCEVXSCHDFMGLNGRLFP----- 823
 QY 1239 DYVIALVFNLENPEGDPLHITIDGRDLSPLIGSFQSOLPGRIBSSNSLFLA----- 1293
 Db 824 -----VNIQLGAKVDVCD-----EGFOLKG--SSASVCYLAQMEST 858
 QY 1294 FRSDASVSNAGFYVDIYENPRESCEPDGSIKNGTRVSGDLKL--GSSVYYVYCH----- 1344
 Db 859 WNSVPCBOIF-----CPSPVLPNGRHGKFLVPPFGKITVYITCDPHPDNG 907
 QY 1345 GGYVEBCTSTLSCILGPDGKPVNNPPVCTABCGQYVSGDGVLSPPNYQNTYSQIQC 1404
 Db 908 TSEDLIGESTRICTSPDQNGWSSPAPRC-----GIL----- 940
 QY 1405 LYEVTVPKOVVFGQFAFFHTALNDVVEVHDGHSQ--HSLILSSLSGSHTEBGLPIATSN 1462
 Db 941 -----GHCOAPDHFLEFAKLTQTNASDPFIGTS- 968
 QY 1463 QVLIKESAKGLAPARGF-----HFYQAVPR--TSATOCSSVPEBRYGK-RLGSFSPVG 1513
 Db 969 ---LKECREPEYGRPRSTICLDNLVWSS--PKOVCKRKSKCTPPDVNGMVAHYITDIQVQ 1024
 QY 1514 AIVREPCNSGYALQGSBEIECLFVPGALQMNVSAPTCV--VPCGMLTERRGTILSPGP 1572
 Db 1025 SRINYSCTTGHRLIGHSSAECI--LSGNAAMHMSKTPICORIPCGLPPTIANGDPFISTNRE 1083
 QY 1573 EPLNLSNCWAKIVVEGAGIQIOVVSFVTEQNMWDLLEVFDGADNVMTLMGSEFSCTIVA 1632
 Db 1084 NFHYGS-----VVTYRCNPGSGGRKVP-----LVGSPS----- 1112
 QY 1633 LUNSTNOLYLFHYSDISVASAGFHLLEYKTVGLSSCEP--AVPS-----NGVKTB 1682
 Db 1113 -IYCTEND-----DQVGIWSPAPQCIIPNKCTPPENENGLVSD 1151
 QY 1683 R---YLVNDVVSQCEPGYALQGHAIISCMPTGVRRWNTPPPLICAQCGGTVBEMEGVIL 1739
 Db 1152 NNSLFLNEVERRCOPFVMKGPBRVVKO--ALNMKBELPSCSRVC----- 1197
 QY 1740 SPGFPGNYPNMDCKWIKALPVGFAGHIOFLNSTEPMNDYIEIRNGPETSMMGRFSG 1799
 Db 1198 -----QPPDVL----- 1204
 QY 1800 SELPSSLSTSHETTVYFHSDSQNRPGKLEVOAYELOECDDPEBFANGIVRAGAYNG 1859
 Db 1205 -----HAERTQR-----DKONF-----SPG 1219
 QY 1860 QSVTFECLPGYOLTHGPVLTQGHGTVRMDHPLPKCEVPCGANTSS--NGTVVSPGSPS 1917

Db 1220 QEVFTSCEBYDLRGASWRT--PDGWSPAAPFCEVKSCHDFMGQLLNGVLPF----- 1273
 QY 1918 PYSSQDCVWLITVPIGHGVRLNLSILOPEAGDEFTIWDGPOQTAPRLGVFTRSMAKKT 1977
 Db 1274 -----VNIQLGAKV-----DVCD-EGFQLKG----- 1294
 QY 1978 VOSSNQVILKPHRDAATGIFALIAFSAVPLTK---CPPEITLPNAEVTTN--EERNIGD 2033
 Db 1295 ---SSASVCVL-----AGMSLWSSVPCBOIFCSPPIVNGRHTGKLEVEFPFGK 1344
 QY 2034 IYVRCLP-----GFTLVGNEILCKL-----GYLOPEGPPICEV--HCPTMELILD 2080
 Db 1345 ANNYTCDHPBDGTSFIDLGESTICTSDPOGNGW--SSPAPRCGLIGHCOA----- 1395
 QY 2081 STGVILSOSYPGSPQFOTCSWLVEBDYNISLTVVEYFLSEKQYDEFEPDPSGOSPL 2140
 Db 1396 -----PD-----HFLFAKLTQTNASDPFIGTSLX 1420
 QY 2141 LKALSGNYSAPLITVSSNSVYLKWS--DHAYNRKGFIRIRAPYCSLPRAPLHGFLIGQ 2199
 Db 1421 YECREPEYGRPSTICLDNLV--WSSPKDYCKRS-----CKTPPPVNGMVHT 1468
 QY 2200 TSTQGGSIHFECNAGYRLVGHSMACITRHPOGYLWSEATPLCOALSCGLPEAPKNGV 2259
 Db 1469 TDIQVSRINYSCTTGHRLIGHSSAECILSGNTAH--WSTKTPICORIFCGLPPTIANGDF 1527
 QY 2260 FG--KEYVTGKAVYSCSEGVH--LOAGAETAECLE--DTLWS-----NR 2299
 Db 1528 ISTNRENFHYSGVVYTRCNLSGRKRFELVEBPICTSDNDQVIMSGAPQCIIPNK 1587
 QY 2300 NVPP-----OCVP-----YTC-----PDVSSIS-- 2317
 Db 1588 CTPPVENGILVSDNRSIPLSINVEVERCQGFVWKGPBRVVKOALNKMBELPSCSRVC 1647
 QY 2318 -----VEGRWRLIFETOYQFOAQLMLICDGYTYTGORVIRCOAMKMSLSDSTPTCRI 2372
 Db 1648 QEPPEILHGEHTPSHQDNFSPQGEVFPYSCPEYDLRGASLHCTPOGWS--PEAPRCAY 1705
 QY 2373 ISC---GELPFPNGHRIIGTLV-YGATAIFSCNSGYTLVGSRYRBCMANG--LWSGS 2424
 Db 1706 KSCDPLQL--PRGRVLPFLNLQLAGAKVSFVDEGFRLLGSSVSHCVLWGMSSLMNNS 1762
 QY 2425 EYRCLAGHGTPEPVPVNGINGE--NYSYVSGVYQCN-----AGRLIGMSVRICQ 2475
 Db 1763 VPVCEHITCEMPBALINGRHTGTSPGDIPLYKEISITCDPBPDMGTNLLIGESTITRICTS 1822
 QY 2476 DHR---WSGKTPFC-VBITCGH-----PGNPVNLTOGDNFNLNDVVKFCVNP 2519
 Db 1823 DPHGNGVWSPAPRCSELSVRAGHCKTPEQFPASPTPIINF-----EPVGTSLNVECRP 1878
 QY 2520 GYMAEGARSOCCLASGQMSDMLPTCRILINCTDPGHQENSVQVLAHSGHRSFCTTYSYR 2579
 Db 1879 GYFGMFSIS--CLENLVWSSVEDNCRRKSCGPPEPFMGVHNTID--TOFSTVNY 1933
 QY 2580 CNHGFYLLGTVLSQCGDG--TWDRPPQCLVASCQHPGSPPHSOMSGDSYT----- 2629
 Db 1934 CNEGFRLLIGSSTICLVSGNNVTWDKAPICEIIS--EPPITISNGDYNNRISF 1989
 QY 2630 VGAVYRISC-----IGKRLVGNSTRMCGLDHWTGSLPHCSGTSVGVCDPG 2677
 Db 1990 NGTVVTVQCHTGPDEQLFELVGERSTY--CTSXDQVGVWSSPPRCISFN--KTAPE 2045
 QY 2678 IPAIGIRLGDG---FDGTVWRFCSEAGHYLRGSEKTCQANGWSSQPECGVISCNP 2734
 Db 2046 V-ENAIRVPGNRFSFSLTEVFRQCPGFVWVSHTVQCTNGWGPCLPHPCSVV-COP 2103
 QY 2735 GTPSNARVFS--DGLVSSSIYVECEGEGYATILSRHSVNGTWTGSPBECLVINGD 2792
 Db 2104 PEILHGEHTLHQNFSPQGEVFPYSCPEYDLRGASLHCTPOGWS--PEAPRCITVXSCDD 2153
 QY 2793 --PGIPANGRLGNDFFYKNTVTVQCVGYMMESHRSV--VLSCXTKRTNNGTVPCVCL 2848

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Db      2164 FLGLPHGRVLLPLNLQLGAKVSFVCDGFRLLKGRSASHVLAQMK-ALMNSSVAVCEQI 2222
Qy      2849 MCKRPPLIPNGKVGS---DPMSSSVTYAC-----LEGYQLSLPAVTCGNG 2894
Db      2223 FCPNPAILNGRHGTGTPPGDIPYKEKISYACDTHPRDMFTNLIG-SSSIRCTSDRONG 2281
Qy      2895 SMTGELPQC---FVFCGDPGVPSRGRREDGFSY---RSSVSFCHPPLVAVGSPRRFC 2948
Db      2282 VMSPPARCELVSVAACDPDPKIQNGHVIIGHVSLYLPGMTIYICDPBGYLLVKGFIYC 2341
Qy      2949 QSDGTWGTGTOPSCIDPLTTCADGVDPQFGIQNN---SQGYOVGSYVLFRCCQKYLQGS 3005
Db      2342 TDQGWISQLDHYCKE---VNCSPF-LFMNGISKELEMKVYHGDYVTLKCEDGYTLGSS 2397
Qy      3006 TTRTCLPRLTWSGTRP 3021
Db      2398 PWSQCQADRRWD--P 2411

RESULT 4
US-09-341-461-2
; Sequence 2, Application US/09341461
; Patent No. 6586389
; GENERAL INFORMATION:
; APPLICANT: Hammond, Timothy G.
; APPLICANT: Verroust, Pierre J.
; TITLE OF INVENTION: Cubilin Protein, DNA Sequences Encoding Cubilin
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: D6148
; CURRENT APPLICATION NUMBER: US/09/341,461
; CURRENT FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: PCT/US99/01259
; PRIOR FILING DATE: 1999-01-21
; NUMBER OF SEQ ID NOS: 40
; SEQ ID NO 2
; LENGTH: 3623
; TYPE: PRT
; ORGANISM: rat
; FEATURE:
; OTHER INFORMATION: amino acid sequence of rat cubilin protein
US-09-341-461-2

Query Match      8.2%; Score 1390.5; DB 4; Length 3623;
Best Local Similarity 20.7%; Pred. No. 6.3e-98;
Matches 702; Conservative 369; Mismatches 1069; Indels 1251; Gaps 130;

Qy      101 NEGYDLOGSKRITCMKVSDFMAVSDHRRPVCRAHCDALHGPSGIIT--SPNFPLOYDN 158
Db      443 NGGTCIDGINGFTC---DCTSSWTGYVCGTPQAACGILSGTGTAYGSPN--DYIG 496
Qy      159 NAHCVMITLALNPKVYIKLAEFPDL-----RGYDTLVGGGQGGDDQKTVLYMSQNA 212
Db      497 NVNCFWIVRT--DEEKVLGVTFPFEDLESANCPREY--LQIGDDSSADPFLGRY----- 548
Qy      213 CSDSPHPGSRIPESMSGDIMRQKMTVLEICRDISSDARSAGSRKSKPTKSNIAELVAPG 272
Db      549 C-----GSRPPGIG-----SSANALYF----- 566
Qy      273 TELGSGCGDPGIPAYGRREGSRFHGDTLKECOPAFELVQKAITCKQNNQMSAKPG 332
Db      567 -----GLYSEYIRSGRGF-----TARWEALKE 589
Qy      333 CVESCFNFTSPSGVLSPNYPEDYGNHLHCVMLILAPBSRIHLAFNDIVDP-----QF 388
Db      590 CGGILTYNNY-----GSITSFGYPGNYPGRDCVMQVLVNPNSLITFTFGTSLSESGNCSK 645
Qy      389 DELVIKDGATAEAVLGTFGSGNQLPSSITSSGHVABLEFOTDHTGKRGENTFTTFRHN 448
Db      646 DYLIRDSPPGQDVLGKFTCSLSLTPPKITGPAPARIGFGSDSETSDKGFITVLTQSD 705
Qy      449 -EC-----DPPGVVNGKR-----FGDS 465
Db      706 LDCGANTDTDGLLPLPLSPFGSGRCVYLITQAGQEQIVINFTGVELSEQMGCGTY 765

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Qy      466 LQIGSSISFL---CDEGFLTGQSETITCVLKSGSVYV-----NSAVLRC--EAPC 511
Db      766 IEVGDGSLRLKLC-----GNETLPPIRSVSNKWIIRLDALYQKASFRADYVAC 817
Qy      512 GGHILTSPTGTLSPGMDGFYKDALSCAMVLEAOPGYDIKTFDFK-----TEVVDYTLVE 567
Db      818 GGMRLG--EGFRRSGFFYNAAPGRATCRMTISQPRQVVLNLFDFQIGSSASACDTYIEI 876
Qy      568 RDGRTYAPLIGYVHGTQVPOFLISTSNVLYLFTDKSHSDIGFQRLRYETITLQSDHCL 627
Db      877 GPSSVLGSPGNEKFCSSNIPSFITSVYNIYLVTFVKSSEMNGFTAKFSDDKLE----- 931
Qy      628 DPGIPVNGQRHNDIFYGALVTFSCDGYTLSDGEPLECEBNPQMSALSCALCGGFI 687
Db      932 -----CGEVL 936
Qy      688 QGSAGTILSPGPDYFPNNLNCWTIIEISHGKGVFFTEHTFHLSEGH---DYLLITENG 743
Db      937 TASTGILIESPGGRVYRGVNCCTMGVVQGRQGLRLRLEFSSFYLEFGVNCNDYIEIDTA 996
Qy      744 SFTQPLRQLTGRSLPADISAGLYGNFTAQVRFISDFSMYSYGFNITSEYDLEPCEBEV 803
Db      997 AQTF-LGRYCGKSGIPSLTS---NSNSIKLIFVSDSALAGEGFSINYEALD----- 1043
Qy      804 PAYSIRKGLQPGVGDITLFCGFPYRLGTAITCLGRRRLMSSPLPRCVABEGNSVTG 863
Db      1044 -ASSV-----CLVYTD 1054
Qy      864 TQGTLSLPNFPVNNNHCEIYSIOTPGKGIQKARAFELSE-----GDVLKVYDGN 917
Db      1055 NFGTLSSPNFPNNYPSWBEICRTTGLNQAIALGFDFLDEFGSQCDVPVIRGCV 1114
Qy      918 NSARLGVFSHSEMGVTLNSTSSSLWLDFTTDAENTSKPELHF----- 962
Db      1115 ETSPLVIGYCG--VLPTTIISGSNKLMLKFKSDALAKFGFSAVWDSSGCGGLNLTTPQ 1173
Qy      963 -----SSEFLICEDGCTPKPGYKXNDDEHFAFGSSVSFSCDDCY----- 1001
Db      1174 VLTSPNYPMPYSGSECYWRLSESGSPFLEFODFLBEGP---SCSLDYLRGVDPPT 1229
Qy      1002 -----SLRGESELLCLSGE-----RRTWRPLPTVAEC 1030
Db      1230 TNSRLIDKLGGDTTPAIRSNKQVVLKTBELWQGLRGFEINFRRCNNV----- 1282
Qy      1031 GGTIVGVSQVLSPGYPAPYENHNLCTIWEAGCTIGLHFLVPDTEV---HDVLR 1086
Db      1283 ---IVNKTFGILBSINYPNPDKNQCNMTIQATTGTVVYTFGLFVDESVMNCSTDYVE 1339
Qy      1087 IMGPVVSQVLLKELSPALPKDLHSTFNSVVLQFSTDFTS--KQGFALQFSVSTATSCN 1145
Db      1340 LYDGPQWNG---RYCANNMPPGATTGSQLGVFGDGINSGKGRKO----- 1385
Qy      1146 DPGIPQNGSRSGSWEAGDSTVFOCDPGVALQGSABISCVKIEHRFPWQSPPTCIAPCG 1205
Db      1386 -----WFTGCG-----CG 1392
Qy      1206 GDLTPSGVILSPNYPPEPPGKCDWKVTVSPDYIALVFNI FNLEPG---YDFLHIY 1261
Db      1393 GEMGTAGSFSSPCYFNSYPGNKECINWIRVAPSSIOITLGDPEVEYGSNCVDSLEIY 1452
Qy      1262 DGRPSLPLGSRFG---SOLPGRIBESSNSLFLAFPSDASVSNAAGVIVIDYTERPSSCF 1318
Db      1453 AGLDENSPRIAQLCSQSPSANPMQVSSVTGELALRFETDSTLNGRGFNASRAVP----- 1507
Qy      1319 DPGSIKNGTRVGSDLKLGSSTVYYCHGQYVEGHTSLSCILGPDGKVMNNPVPVCTAPC 1378
Db      1508 -----CG-----C 1510
Qy      1379 GGOYVSGDGVVLSBNYPONTSGQICLYEYTVVK--DYVFGQAFFTALNDVVEVHDG 1437
Db      1511 GGIQLSRGIBSNYPNNYRANTECSMIIQVERGAVLLNITDFTLEADPSCLRLMDGS 1570

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QY	1438	SOHSLRLSLSSGHTSESLPLATSNQVLKFEFAKGLAPRGHFYQAVPRISAQCGSV	1497
Db	1571	SSSTNARVAVACGRQCPNNITIASGNSLFRFRSSGSSQNRGRAFRE	1618
QY	1498	PEPRYGRKIGSDPSGVAIVRECNNGVALQSGPEIECLPVPGALQMVNSAFTCVVPCGG	1557
Db	1619	-----FCGG	1622
QY	1558	N-LTERRGITLSPGPEPEYPLNSLNCVWKI-VVPEGAGIQIUVSF-----VHEQWMDSLV	1611
Db	1623	RMTDBSDPTIFBPLPGNYLGNQNSMIIEAOPPRNGITLSTGTQOLONSTDCTRDFEII	1662
QY	1612	FDGADNTVYMLGSGFGTTPVALLNSTNOLYHAFYSDISVSNAAGFHEKTVGLSSCPER	1671
Db	1683	LDGNVDYDAVQRCGFSPLGPBIIISFGNALTVRFVTDSTRSPREGRAIYSA-----	1733
QY	1672	AVPNSGVCKTGERIYLVNDVVSFOCEBEGYALQHAHISCMPTVRRNNYPRPLICIAOCCGTV	1731
Db	1734	-----STSCGGSF	1742
QY	1733	EEMEGVILSPGPEPNYPNSMDCSKIALPVGFGAIIQIINFSTED-----NHDIYIRRG	1787
Db	1743	YTLDDGFNSPDVFPADYGPRAEVMNIIASPGRRILDSLSPNLESLNCKMDFVIRGC	1801
QY	1788	YETSRMGFRGSGSELPSLLSTSHETT-VYFHSQNRPGFKLEYQ-----	1833
Db	1802	NATGGLIGYCCNSLPGNVSSAEGSGLWVRFPVSDSGTGMGFOARFNNIIVGTGG	1861
QY	1834	AVELQCEPDPEF-----ANGIVRGVNVGOSVTFECL-----PGQULGH	1875
Db	1862	KIASFWGKRYNYSNKKVNVAVDAGIIGRILEMDIEPTTNCYDSLKYDDGF-TGS	1920
QY	1876	PVLTQCHT-----NRNW-----DHLPRCEVP--CGG	1901
Db	1921	RIGTYCQTQTESFSSRNRYLTFOPSSDSVSGRGLFEMFVAVDVSDSTPRTIAPGACGG	1980
QY	1902	NITSSNGTV--YSRPFSPYSSODCWLLIWPIGHGRNLSLLOTER---SGDFTI	1955
Db	1961	FMVTDDBTEGIFSPGMPREYANAGACIMIIYAP-DSTELNILSLDIEPQSCNYDKLIV	2039
QY	1956	WDGPOOTAPRLGVFTSRMAKKTVOSSNOVLKFRHDAATGIFAIAFSAVPLTKCP--	2012
Db	2040	KDGDSDLPBLAVLGVSPGPIRSTGVMYIRFSDISVAG--TGNMAFGSGCGYL	2096
QY	2013	-----PPLIINAEVYVNEEFNIGDIYRVCLEPFTL-----VGNELI	2051
Db	2097	GADRGVITSPKYPDYILPNLNC-----SWGVLVQ--TGLTAVGFEOPFOIQRNDS	2145
QY	2052	TCKLGTVLOF-----EGPPI-----GEVHCPF--NELL-----	2078
Db	2146	FCSQGDYVLVLANGPNPSPLGPGSRNRPFGCMVAPSTLFTSGNEMFPOQFISDSNGCG	2205
QY	2079	-----TDSGTGVLISQSYPGSPYPOQTCSMVVRVEDYNISLVEY	2118
Db	2206	FKIRYEAKSLACGTVYIGDADSDGYLSPYVPYANYPQAGACIMILEAPGRSIOLOFE	2264
QY	2119	FLSEKQYBEFELPDGSPGSPILKALSG-NYSAPLIV-----TSSNSVLRMS	2166
Db	2265	-----DQFIEDTPNCVSYLELRDANSNARKVSKLCCGTLPGSWSSRERTYIKFG	2317
QY	2167	SDHAVNRKGFIRIRYAPYCSLPRAPLHGFILIGOTSTOPGSGIHFCNAGYLVGHSMAIC	2226
Db	2318	TDGGSYVWGFAKXSIAAC-----GRTVSGDSGVTE-----	2348
QY	2227	TRHROGTHLMEBALPLCALSCGLPEAPKMGVGEKEYVTGKAVY--SCSEGYHLOAGA	2284
Db	2349	-----SIGYPTLFPYANNVCQWFIRLPGGYLTLSPEDFNLOSSP	2388
QY	2285	EATAECDLDTGLMSN-----RNVPCQCVPTCEPVSI-----SYEHGRKMLIF	2327
Db	2389	GCTDQFVE--IWEHGTSRVLGRVCGNSTPESVD-TSSNNAVSVFVTDGVSATSGAFLOF	2445
QY	2328	ETQYQFQAQMLICDPGYTTYTGQVIRCOANGKMSLGDSTPTCKRIISGELPILPBNHRI	2387

Db	2446	KSRQ----	VCG-----	GDLCGPTG--	FTSPNYPN	PGARI	2477
Qy	2388	--GTLVYGATAIF-----	SCNSGYTLVGSRV	ECMANGTMSGSEVR	CLAGHC	2433	
Db	2478	CEMTITVQEGARRIVLTFTNLR	LTSTQSPCNSGCLIV-----	PNGRJNS	-----	2520	
Qy	2434	GTPBYNGHINGENSYRGSVYQ	CNAGPRLIGMSVRICOQ----	DHHSGTKPCPV	2488		
Db	2521	-----PLIO-----	KLCSRVVNTVEFKSGTMYKVF	2547			
Qy	2489	ITCGHPGVNGLTQGNQFNLDVYKVCN	PGVYABGAASQCLASQMSDMLPTCR	ILN	2548		
Db	2548	FTDG--SRPYGGFT-----	ASTSTEDAVCGG--	FLPSVSGN	2581		
Qy	2549	CTDPGHOENSVR-----	QVHSGPHRESFGTTVYRCNHGFFLGT	PVLSQO-----	2595		
Db	2582	FSSRGY--NGRQDVARNLDC	EMTILSNRNRENSISL-----	YFELSTESQDCTFD	2631		
Qy	2596	-----GDGTWDRPPOCLLVSCG	PHSPSQ-----MSGD--SYTVGA	VWYRS--CT	2639		
Db	2632	VLEFRVGDADGRLIEKFC	SLAPAPLVIYYPQWIRFVSENERVEY	T--GYIEXSF	PDGC	2690	
Qy	2640	GKRT--LYNGSTMCGLDGHMGS	SLPHCS-----GTSVGVCGDPGL	PAIGIRL	IGDS	2688	
Db	2691	GIRGNDGVSIPNYPNLYSAMTG--	CSWLLKABEGT-----ITL--	2729			
Qy	2689	FDPQTVARFSCGAGHVLRGSS	ERTCOANGSMGSOPECGYISGNP-----	GTPSNARVY	2743		
Db	2730	-----TLDDFLLEAGPTC--	TSDSVYVANGSPS--PYIGY--CGQSP	RRIRIGSSNOLIV	2781		
Qy	2744	FSDGLVSSSIVYECREGYAT--	GLLSRHCSVNGT-----WTGSDP	-----CLVI	2788		
Db	2782	-----TENTNMQGQTR--	GFYATWTNALGCGGTFGSANGT	IKSPGMQTPPENSRC	SMWY	2835	
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Db	2836	ITGD-----SKGWEISF	SPSNFRIPSSDSQCONSFV-----	KWQGR	LMINKT	2877	
Qy	2848	LMC-----KPPRLIPNGK	VGSDFMMGSSVTYAACLEGYQLSL	PAVFTC--	-----GNGSWT	2898	
Db	2878	LHARSQCDVAPSP	PLVTSGN-----FTAVPQSE	MAAQFSAS	2915		
Qy	2899	ELPQCFEVPFCGDPG--	VPSRGRRDRGFS-----YRSVS	PSCHPPLVLV	2942		
Db	2916	FISRCGRFTMSPDRI	ISPNFQYDNNMCTYLADPQSVIL	FRVSGLEDR	SAITG	2975	
Qy	2943	SPRPFQSDG-----	TWSGTQ-----PSCID--PULTT--	CADPGVQF	QNN	2982	
Db	2976	T-----CGDGLG	ITKGNLSTPLVITCGSETLR	PLTVGDFVLNFYS	DAVYTD	FGFKIS	3031
Qy	2983	SOGVQVSTVLFRCQKGYLL	QGSTTRCJPN	3013			
Db	3032	YRAITCGG--TYN	SGILRSPSYISNYPN	3060			

RESULT 5
US-09-612-314A-52
Sequence 52. Application US/09612314A
Patent No. 6713606
GENERAL INFORMATION:
APPLICANT: SMITH, RICHARD ANTHONY GODWIN
APPLICANT: DODD, IAN
APPLICANT: MOSKAKOWSKA, DANUTA EWA IRENA
TITLE OF INVENTION: CONJUGATES OF SOLUBLE PEPTIDIC COMPOUNDS WITH
TITLE OF INVENTION: MEMBRANE-BINDING AGENTS
FILE REFERENCE: 37945-0004
CURRENT APPLICATION NUMBER: US/09/612,314A
CURRENT FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 09/214,913
PRIOR FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: PCT/EP97/03715
PRIOR FILING DATE: 1997-07-08

PRIOR APPLICATION NUMBER: GB 96 148 71.3
PRIOR FILING DATE: 1996-07-15
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 52
LENGTH: 1947
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: CRI
US-09-612-314A-52

Query Match 8.1%; Score 1375; DB 4; Length 1947;
Best Local Similarity 22.0%; Pred. No. 3.5e-97;
Matches 540; Conservative 267; Mismatches 842; Indels 810; Gaps 109;

798 CEEBEVPA--YSIRKGLQFGVDTLTFSCEPGYRLGRTARITC-LGRRRLMSSPLPRC 853
63 CRNPDPDVGNGVHVIKGIQF--GSQIKYSCTKGYRLIGSSSATCIIISGDTVIMNETPIC 120
854 -VAECGNSVTCTGTLSPNPVNNNHCEIYSIQOPGKIQDLKARAFELSGDVLKV 912
121 DRIPCGLPPTTNDGFISTN--RENPHYGSVVTYRCNPGSG--GKRVFEL-VGEP-SI 172
913 YDGNNSARLGVFSEHMGVTLNSTSSLMDFITDAENTSXGFEHFSSFELICED 972
173 YCTNSDQ--VGIMSGAPQCIIPN-----KCTP 199
973 PGTPEKFGYKVDHGF--AGSSVSFSCDPGYSLGSEELLCLSGERTWDRPLPTCVAEC 1030
200 PNVEN-GILVSDNLSFLNEVEFRCOPGFVMKGPVRKQALNK--WEDLPSCSRVC 256
1031 GGYRGEVSGQVLSPGYAPAEHLNCLITWEAAGCTIGLHFLVPTDEVDLRLWDG 1090
257 -----QPP-----DVLH----- 264
1091 PVESGVLLELSPALPDLHSTFNSVVLQFSTDFTSKQFAIQFSVSTATSCNDGIP 1150
265 -----A 265
1151 QNGSRGSDSWAGDSTVFOCDPGYALOGSABISCVKIENRFWQSPPTCIAPCGDLTG 1210
266 ERTQRDKNFSPQGEVFSCEPGYDLGASMRCTPOD--WSPAPTCGVKSCDDPMG 322
1211 P--SGVLSPPYRPPYRPGKCDMKVTSPPYVALVFNLENPEPGVDFLHIYGRSLS 1268
323 QLNLGRVLP-----VNLQLGAKVDFVCD----- 346
1269 PLIGFSYGOLPGRIESSNSLFLA-----FRSDASVNAAGFVIDYENPRESCFDPGSI 1323
347 -----EGFOLKG--SSASVCYLAHMSLSNVSVPCEQIF-----CPSPFVI 386
1324 KNGTRVSGDLKL--GSSVTYYCH-----GQYVEGSTLSLCLGPDGKVMNNPVPVC 1374
387 PNGHGTGKPLEVFPFGKAVNYTCDPHDRGTSFDLIGESTIRCTSDQNGQWMSPPARC 446
1375 TAPCGQYVSGDGVVLSBNYFQNTSGQICLYFTVPRDYVVFQGFAPFTALDNDVEVH 1434
447 -----GIL----- 449
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450 -GHQADHFLFALTKQTOTNASDFIGTS--LKTGCRPEYGRPESITCLDLWVSS- 503
1487 PR--TSATQCSSEVEPRYK--RLGSDPSVGAIVFECNSGYALOGSBEIECLPYVGAIAQ 1543
504 PKDVCXKSKCTPRDPVNGVHVIITDIQVGRINYSCTTHRLIGHSSABEIT-LSGMAH 562
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1603 EQMWDSELEVFDGADNTVTMLGSPSGTIVPALNLSNQLYLHFYSDISVSAAGPHLSYKT 1662

605 NPGSGKRYFE-----LVGDS-----ICTSND-----DQ 630
1663 VGLSSCEP--AVPS-----NGVTKGR--YLNDVVSFQCEGYALQHAHLSM 1709
631 VGIMSGAPQCIIPNKCTPRNVENGILVSDNRSLSFLNEVEFRCOPGFVMKGPVRKQC 690
1710 PGYVRBNVYRPPICIAQCGGTVEEMEGVILSPGPNYPSNMOCMKIALPVGCAHIQF 1769
691 --ALNKKPEELPSCSRVC----- 706
1770 LNFSTERNHDYIEIRNGPYETSRMNGRSGSELSLSLSTSHETTVFHSDSQNRBGF 1829
707 -----QPPPVVL-----HARTQR----- 720
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721 -----DKDN-----SPQGEVFSCEPGYDLGASMRCT--PQGDWS 756
1890 HPLPKCEVPCGNGNTSS--NGTVYSPGFSPYSSQDCWLLTPYIGHVRLNLSLQTE 1947
757 PAAPTCGVKSCDDPMGQLNGRVLP-----VNDQLGAKV----- 791
1948 PSQDFTITWDGPOOTAPRLGVFTSRMAKTVQSSSNQVLKFKHDAATGIFAIAFSAYP 2007
792 --DFVCD-BGFOLKG-----SSASVCVL-----AGMESLMSNSVP 823
2008 LTK--CPEPTILPNAEVTEN--EENIGDIYRYCLP-----GPTLVGNELITCKL-- 2055
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2056 --GTLYQFEGPPICEV--HCPTNELLTSTGVILSQSYRGSYPOQOTGSMVLRVBPDY 2110
884 QNGVW--SSPAPRCILGHCOA-----PD- 906
2111 NISLTVYFLSEKQYDFEIEFDPGSGQSLKALSGNYSAPLIVTSSNSVYLRMS--DH 2169
907 -----HFLFALKQTQNASDPIGTSLKRYEGRPYGKPFSTICLDNLV--WSSPKD 956
2170 AYNRKGFKIRYSAPYCSLPAPLHGLTQSTQPGSHPFGCNAGYRLVGHSMATGRH 2229
957 VCKRKS-----CTPRDPVNGVHVIITDIQVGRINYSCTTHRLIGHSSABEILS 1007
2230 PGYHLMSEALPILOALSGLPEAPKMGVFG--KEYVTGTAYVSCSGSYH--LQA 2282
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2283 GAETAECL-----DTGLMS-----NENVP-----QCV 2306
1067 VGEBSITCTNDNDQVGMSPAPQCIIPNKCTPRNVENGILVSDNRSLSFLNEVEFRCQ 1126
2307 P-----VTC-----PDVSSIS-----VEHGRWLLFETOYQOALMLICD 2342
1127 PGFVMKGPVRKQALNKKWPELPSCSRVCQPPPEILHGHNTSHQDNFPGQEVFSCE 1186
2343 PGYTYGQRIYRQANGKSLGDSPTPTCTIISC--GELPIPNGRIRIGTSLV-YGATA 2397
1187 PGYDLRGAASLHCTPQGDWS--DEAPRCVAKSCDDFLGQI--PHGVLPFLMLQLGAKV 1241
2398 IFSCNSGYTLVGSRVRECMANG--LWSGSEVRLACHGCTPPEIYVNGHNGE--NYSY 2451
1242 SFVCDSEFRALKSSVSHICVLVGRSLMNSVPRVCEHIFCNPRAIILNGRHTGTPSGDIPY 1301
2452 RGSVYQCN-----AGFRLLGMSVRIQQDDH--WSGKTPTC-VPTTGH----- 2493
1302 GKEISYTCDBHPDRGMTFNILIGESTIRCTSDPHNGVWSPAPRCSELSVAGHCKTPEQF 1361
2494 -----PGNPVUGLQGNQFNLDVVKYVNGVGAABGAABQCLASGQMSMLPTCRINC 2549
1362 PFASTPIINDP--EFVGTSLNIECRGYYGKMFESIS-CLENLWSSVEDNCRKSKC 1416
2550 TDPGHGENSVROYVNASGPHRFSGTIVSYCNHGFYLLGTPVLSQCGD--TWDRRPQ 2606

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Db 1417 GPPPEFNGVHINTD-----TQFGSTVYVNSCNEGFRLLGSPSTCLVSGNNVTDKAP1 1472
Qy 2607 CLVSCGHPGSPPHSOMSGDSTY-----VGAVVRYSC-----IGKRTLVGN 2647
Db 1473 CEIISC-----BPPETISNGDFYSNNKRTSFHNGTAVVYQCHTGPDEQLFEIYGRS1Y-- 1526
Qy 2648 STRMGCGDGHWTGSLPHCSGTSGVCGDPG1PAHIGLIGDS---FDPGVRFSCEAGHY 2704
Db 1527 CTSMDODGVWSSPPRCIS1TN--KCTAPBY-ENAIKVPGRSFFSLTEIRFCQPGFV 1583
Qy 2705 LRGSSERTQANGWSSSQPECGV1SCGNPGTSPMAVVS--DGLVFSS1VYECREGY 2762
Db 1584 MVGSHTVQCCOTNGRMGKYLPHCSRV-CQPPETI1HGHNTLSHQNFSPGGEVFSCPSY 1642
Qy 2763 YATLLRHCSTVNGTWSDECIYVNGD--PG1PANGRLGNDPFRYKTYVYQCVPGY 2820
Db 1643 DLRGASLHCTPQGDWSPPEARCTVKSODFLQGLPGRVLLPLNTQLGAKVSVCDGEGF 1702
Qy 2821 MESHRSV--VLSTCKRTWNGTKPVCKALMCKPPL1PNGKVVS---DEMGSSVTVY 2875
Db 1703 RLKGRSASHCYLAGMK-ALMNSVVPCEQ1FCBP1ALNGRHTGTFRGDI1PYGKE1S1Y 1761
Qy 2876 C-----LEGYLSLPAVFTCEGNSWTGELPQC--PVPFCGDPVPSRGRRED 2921
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Db 1821 GHVSLY1PGMT1STTCDPGYLVGKGFT1CTDQ1MSQLDHYCKE--VNCSPF-LFMNG 1876
Qy 2979 IONN---SOGYOVGTVL1FRCOKGYLLQGSTTRTCL1PNTWSGTPPDCV--PHHCRPOE 3032
Db 1877 ISKELEMKYVHYGDYVTLKCEQGYTLGSGPWSGCCQADRM1PLAKT1SRA1CCDGPX 1935

RESULT 6
5256642-2
Patent No. 5256642
APPLICANT: FEARON, DOUGLAS T.; KLICKSTEIN, LLOYD B.; WONG,
MINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F., JR., STEPHEN
H.; MAKRIDES, SAVVAS; MARSH, HENRY C., JR.
TITLE OF INVENTION: COMPOSITIONS OF SOLUBLE COMPLEMENT
RECEPTOR 1 (CRL1) AND A THROMBOLYTIC AGENT, AND THE METHODS OF
USE THEREOF
NUMBER OF SEQUENCES: 30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588,128
FILING DATE: 24-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 412,745
FILING DATE: 26-SEP-1989
APPLICATION NUMBER: 332,865
FILING DATE: 03-APR-1989
APPLICATION NUMBER: 176,532
FILING DATE: 01-APR-1988
SEQ ID NO:2
LENGTH: 2039
5256642-2

Query Match      8.0%; Score 1362; DB 6; Length 2039;
Best Local Similarity 22.0%; Pzed. No. 3,9e-96;
Matches 537; Conservative 266; Mismatches 833; Indels 810; Gaps 109;

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Qy 1031 GGTVRGEVSGVLSRGYPAPEYHN1NCWT1EABGCT1GLHPLVFDTEVHDL1RWDG 1090
Db 298 -----QPP-----DV1H----- 305
Qy 1091 PVSGV1L1KELSGPALPKD1HSTFNSVVLQFSTDFTSKQGA1QFVS1STATSCNDPG1 1150
Db 306 -----A 306
Qy 1151 QNGSRSGDSWEAGDSTVFCDDGYALQGSAB1SCVK1ENRFPWQPSPTCIA1PCGDDL1G 1210
Db 307 ERTQDKDNFSPQGVFVSCBPGYDLRGASMRCT1PQGD--WSPA1PCEVKSODDFMG 363
Qy 1211 P--SGV1LSPN1PEEYPRCKECDDMKVTVSPDYV1ALVFN1FVLEPGYDFL1YDGRDLS 1268
Db 364 QLLNRGRV1FP-----VNLQ1GAKVDFVCD----- 387
Qy 1269 PL1GSFYGSQLPGR1ESSNS1FLA-----FRSDASVSNAGFVIDYTENPRES1CFDPS1 1323
Db 388 -----EGFQ1KG--SSAS1CVLAGMES1WNS1VPCEQ1F-----CSPPV1 427
Qy 1324 KNGT1VGS1DK1--GSSV1TYCH-----GGYE1GT1SLCT1GPDGK1PWN1PRV1C 1374
Db 428 PGRHTGT1P1E1FPPGKAVNY1CD1HPD1RGT1SFD1IGEST1R1CTSD1PQNGWSS1PABRC 487
Qy 1375 TAPCGQYV1VSGD1V1SNY1PQNTY1SGO1CLY1V1VP1DYV1VFGQ1F1P1H1ALNDV1BVH 1434
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Qy 1435 DGH1Q--HSRL1SLSGH1TES1PLAT1NOV1L1KFS1AK1APAR1G1F-----HFVQ1AV 1486
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Db 646 NPGSG1K1V1FE-----LVGEP1S-----1YCT1SD-----DQ 671
Qy 1663 VGL1SC1P1P1--AVPS-----NGV1KTGER--YLVNDV1VS1FOCE1PGY1ALQ1G1H1AIS1CM 1709
Db 672 VG1WSG1PAP1Q1T1P1K1CTP1PVN1ENG1L1VSD1R1SLF1SLNEV1VER1CQ1P1GV1K1G1RR1V1CQ 731
Qy 1710 PGTV1R1M1V1P1P1L1C1A1OC1G1TVE1MEG1V1L1SPG1P1V1SNM1DS1MK1AL1PV1G1AH1Q1F 1769
Db 732 --ALNKM1E1P1L1P1SG1SRV1C----- 747
Qy 1770 LNF1ST1P1NH1DY1E1LR1NG1B1E1Y1T1SR1MG1R1P1SG1SEL1P1SSL1T1SH1ET1TV1F1H1SD1H1Q1NR1G1FK 1829
Db 748 -----QPP1DV1L-----HAERTQ1R----- 761
Qy 1830 LEYQ1V1ELQ1E1CP1D1P1EP1F1ANG1IV1R1AG1V1N1G1S1V1F1E1CL1PG1Q1L1GH1V1L1T1Q1H1T1NN1WD 1889
Db 762 -----DKDN1F-----SPQGV1V1S1CE1PGY1DL1RGA1SM1R1CT--PQGD1WS 797
Qy 1890 HPL1R1CE1VP1CG1N1T1TS--NGTV1SPG1F1PS1B1VS1SS1QD1CW1L1T1P1IGH1GY1AL1N1SL1Q1TE 1947
Db 798 PA1P1T1CE1V1K1S1CD1P1W1G1L1NG1R1V1L1F-----V1N1Q1L1AK1V----- 832
Qy 1948 P1SG1F1T1I1W1D1P1Q1T1AR1L1G1V1F1TR1SM1AK1TV1Q1SS1NOV1L1K1F1H1DA1T1G1I1PA1F1A1FS1NP 2007
Db 833 ---DFVCD-BGFQ1KG-----SSAS1CVL-----AGM1ES1L1N1SS1VP 864

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Db	865	VCEQIFCSPSPVILPGRHGTGRPLEFPFGKAVNVTCDHPDRGTSFIDLIGSTTRCISDP	924
QY	2056	---GTYLOFEPBPPICEV--HCPTLELLTDSGTVLISQSYGSYPOFQTCMILVREBDY	2110
Db	925	QGNQWV---SSPAPRCGILGHQCA-----	947
QY	2111	NISLVEFLESEKQYDEFETFDGSGGSPPLKALSGNYSAPLIYTSNSNYLRMS- DH	2169
Db	948	-----HFLPAKTKQTQNMADPFRIGTSLKYCEBPEYGRFSPITCLDNLV---WSSPKD	997
QY	2170	AYNRKGFIRYSAPYCSLPRAPRLGFIIGOSTPOGGSIHFGCNAGYRLVGHSMALCGRH	2229
Db	998	VCKRKS-----CKTPRPPVNMGMVITIDIOGVSINISCTTGHRLLHSHSABCLLS	1048
QY	2230	POGYHLMSEALPLCOALSCLGPEARKGMVFG--KEYVTGKAVYSCSEGYH-----LQA	2282
Db	1049	GNTAH-WSTKEPPIQORIPCGPRTIANDFISTRNENHYGSVVTYRCNLGSRGRKAFEL	1107
QY	2283	GAENATBEL-----DTGMS-----NRVVP-----QCV	2306
Db	1108	VGEBSIYCTSDDOGVIGWSPAPOCITPNKCTPRVENGLIVSDNRSLFSLNEVVDPRCQ	1167
QY	2307	P-----VTC-----PDVSSIS-----VEHGRWRLIFETQYCFQAOILMID	2342
Db	1168	PGFWKQGRVARKCOALNKEPHELPSCSNVQCPREILHGEHTPHQDNFSGCEVFSCE	1227
QY	2343	PGYITTGORVIRCOANGKWSLGDSTPTCRITSC---GELPIPRNGHRIGLTVS-YGATA	2397
Db	1228	PGYDLRGASLHCTPQGDMS--PEAPRCAVXSCDFLOOL---PHGRVLPELNLQLGKV	1282
QY	2398	IFSCNSGYTLVGSRYRECMANG---LWGSSEVRCIAGHCGRPEPLVNMHINGE---NYSY	2451
Db	1283	SFVCDGEGRLKSSSVSHCVLWGMSSLMNWSYPVCEHTICPNRPAILNGRHTGTSGDILPY	1342
QY	2452	RGSVVYOCN-----AGFRLLIGMSVRLCQODHH-----WSGKTPRC-VBITCGH-----	2493
Db	1343	GKEISYTCDDPHPRDGMTEFNLIIGESTIRCTSDPHNGWVMSAPARCELSVRAGHCKTPBOF	1402
QY	2494	----RGNVYNLUTGQNOFNLDVVKVFNPCPYMAGARSCCLASGOMSDMLPTCRILNC	2549
Db	1403	PPASPTPIINDP---EPVGTSLNVECRPYFGGMEFIS-CLNLUWSSVEDNCRKRSK	1457
QY	2550	TDPGHOENSYVQVHASGPHRFSPFGTTVSYRCNHFYLLGTVLSQSGDG---TYDRBPQ	2606
Db	1458	GRPEPRFNGWHIMTD---TQFSTVYVSCNEGFRLLGSSITTCIVSGNNVTMDKAPI	1513
QY	2607	CLLVSCGHPGSPPHSQMSGDSYT-----VGAVVRYSC-----IGKRTLVGN	2647
Db	1514	CEIISCS---EPPRTISNGDFYSNNKRTSFMHGTVAITYOCHTGRDGBOLFELVGRSRIY-	1567
QY	2648	STRMCGLDGHTGSLPHCSGTSVGVCGPGLPAHGIRLGDS---FEDGTWRFSCBGMV	2704
Db	1568	CTSDODDQVWSSPPRPCLISTN--KTAPEV-EKAIKPRKRSFSLTEIIRFCQGPBV	1624
QY	2705	LRGSSERTQANGSMWSGQPECGVISCNPCTPSNARVVS--DGLVFSSSIYECREGY	2762
Db	1625	MYGSHTVQCCQTNNGWRPLPHCSRV-CQRPPEILHGEHTLSHQNFSPQGVFVSCBPSY	1683
QY	2763	YATQLLSRHGCVNGTWGSDPECLVINGD--PGIPANGGLANDFRNKTYTYQCPGY	2820
Db	1684	DLRGASLHCTPQGDMSPEARCTVKS-CDDBLQGPHEGRVLLPYNLQIGAKVSVPCDEGF	1743
QY	2821	MMESHRVS--VLASTKORTANGTSPVCKALPKCKPPLIPNGKVGS---DFMSSSVTYA	2875
Db	1744	RLKGRSASHCVLAGMK-ALMNSVYPVGQICPNRPAILNGRHTGTGPDILPYKEIESTYA	1802
QY	2876	C-----LBGYQLSLPAVFTCSBNGSVTGBLPQC---PFVFGCDPEVPSRGRRED	2921
Db	1803	CDTHPRDRGMTNLLG-EBSIRICTSDPQNGWVSSPAPRCSELVSAA-CPHPRKIONGHYIG	1861

QY 2922 RGFEY---RSSVSSCHPELVVGSRRFCOSDGTSGTQSPSCIDPLITTCADGVQFG 2978
 DB 1862 GHVBLVPLPGMTISTITCOPGYLVKSGKFTFCTDQSIWSQLDHYKXE---VNSFP-LFMWG 1917
 QY 2979 IQNN---SOGYOVGSYVLFRCONGYLLQGSTTTRTCLPNTLWMSGTP 3021
 DB 1918 ISKELEMKVYHYGDYVTLKCEGDGYTLGSGSPWSCQADDRND--FP 1961

RESULT 7
 5472939-2
 Patent No. 5472939
 APPLICANT: FEARON, DOUGLAS T.; KLICKSTEIN, LLOYD B.; WONG,
 WINNIE W.; CARSON, GERALD R.; CONCIO, MICHAEL F., JR., STEPHEN
 H.; MARKIDES, SAVVAS; MARSH, HENRY C., JR.
 TITLE OF INVENTION: METHOD OF TREATING COMPLEMENT
 MEDIATED DISORDERS
 NUMBER OF SEQUENCES: 30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/138,825
 FILING DATE: 19-OCT-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 588,128
 FILING DATE: 24-SEP-1990
 APPLICATION NUMBER: 412,745
 FILING DATE: 26-SEP-1989
 APPLICATION NUMBER: 332,865
 FILING DATE: 03-APR-1989
 APPLICATION NUMBER: 176,532
 FILING DATE: 01-APR-1988
 SEQ ID NO:2
 LENGTH: 2039
 5472939-2

	Query Match	8.0%;	Score 1367;	DB 6;	Length 2039;
	Best Local Similarity	22.0%;	Pred. No. 3.9e-96;		
	Matches 537;	Conservative 266;	Mismatches 833;	Indels 810;	Gaps 109;
Oy					
Dd					
Oy	798 CEEBEVA---YSIRKLOFGVGDTLTFSCFPYRLGTRATC-LGRRRLWSSPLRC	853			
Dd	104 CRNPDPVDNMGWHYIKIGIQF--GSQIKYCKTKGRLLGSSSATCIIGSDIVIMNERPIC	161			
Oy	854 -VAECGNSVTGTGGTLLSPNFPPVNYNHNECTIYSIQTOPKGIIQLKARAFELSEGDVLKV	912			
Dd	162 DRIPCGLPRTITNGDFTSTN---RENPHYSVVTVYRNCNPSG--GRKFVEL-VGSD-SI	213			
Oy	913 YDGNNNSARRLLGVSHSHEMMCVLTANSTSSSLMDFTIDAENTSKEGFELHSFFELTCED	972			
Dd	214 YCTSNDQO--VGISGAPAOCCIIPN-----XCTP	240			
Oy	973 PGTPCFGYKHYDEGHF--AGSSVSFSDDPGYSLRGSELCLSGERTWDRPLYCYAEC	1030			
Dd	241 PNVEN-GILVSDNRSLFSLNEVFERRQPFPVMKGPFRVVCQALNK--WEBELPSCGRVC	297			
Oy	1031 GGTVRGEVSGOVLSPGYPARYEHNLCIMWTIEACCTIGLHLVPFDVEEVHDVLRIMDG	1090			
Dd	298 -----QPPP-----DVLIH----	305			
Oy	1091 PVESGVLLKELSGPALPKDLHSTFNSVYLQFSTDFTSKOGFAIQFVSSTATSCNDPCIP	1150			
Dd	306 -----A	306			
Oy	1151 QNGSRSGDSWEADGSTVFOCDPGYALQGSABEISCVIENRFPMQSPPTCIAPOCGDLTG	1210			
Dd	307 ERTORDKDONSPPGOEVYVYSCBPGIDLGAAISMRCCTPGCD---MSPAAPTEVKASCDDFMG	363			
Oy	1211 P-SGVILSPNYPEBPYPGKCEMKVTSBDYVALVFNIFNLBPGYDFLHIYDGRDSL	1268			
Dd	364 QLNLGRVLFP-----VNIQLGAKVDFVCD-----	387			
Oy	1269 PLISPFYGSQLPRIBESSNSLFLA----FRSDASYSNAGFYVIDTYENRESGCFPDGSI	1323			
Dd	388 -----EGFDLKG--SSASYCVLAGMESLMNSVPCEIOF-----CPSPPIV	427			

QY 1324 KNQTRVSGDJKL---GSSVYTYCH-----GGYEVEGTSILSLGPDGKPVNNPPVC 1374
 DB 428 PNGRHTCKPLEVFPFGAVNYTCDPHDRGTSPLIBESITIRCTSDQNGVSSPAPRC 487
 QY 1375 TAPCGGYVSGDVLSPPNYPONTSGOICLYFVTVBKDYVFGPAFHTALNDVEVA 1434
 DB 488 -----GIL----- 490
 QY 1435 DGHSG---HSRLSLSSGSHGSELPLATSNQVLKESAKGLAPARGF-----HPVQAV 1486
 DB 491 -GHQADPHFLPALKTQTNASDPRTGTS---LKECREPYGGRPSITCLDNLWSS- 544
 QY 1487 PR---TSATQCSSVDEPRYK-RLGSDFSVGAIVAFECNSGVALQGSPEIECLFVPGALQ 1543
 DB 545 PKOVCKRKSCKTPDPVNGVHVITDIOVSRINYSTCTGHRLLGHSSACCT--LSGNAH 603
 QY 1544 MNVSAPTCV-VPCCGNITERGTLISPGPEPYLNSLNCWKIVPEBAGIQTIVVSFTV 1602
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 DB 732 --ALNKKPELPSCSRVC----- 747
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 DB 748 -----QPPDVL-----HAERTOR----- 761
 QY 1830 LBYOAVELQECRDEPFPANGIVGAGYVQSVTFECLPGYQUTGHPVLTCQHATRNMD 1889
 DB 762 -----DKDN-----SPQEVFYSCEPQYDLRGAASMCCT---PQDMS 797
 QY 1890 HPLPKCEVPCGAGNITSS--NGTYVSPGSPSYSSODCVLITVPILGHGVRLNLSLQTE 1947
 DB 798 PAAPTECVKSCDDPFMQLNGRVLFP-----VNIQIGAKV----- 832
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 QY 2008 LTK---CPPTILPNAEVVTEN--EEFNIGDIVRYCLP-----GFTLVGNEILTCCL-- 2055
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 QY 2056 ---GTIYQFEGPPICEV--HCFPTNELLDSTGVILISQSYPGSPQGFQTSMLVREPDY 2110
 DB 925 QGNGVW---SSPAPRCGILGHCA-----PD- 947
 QY 2111 NISLVEYFLSEKQYVEFEIFDGPSSGOSPLKALSGNYSAPLIVTSSNSVYLWMS-DH 2169
 DB 948 -----HFLPAKLTQTNASDPRTGTSKYBCRPYEGFBSITCLDNLV--WSSPD 997
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 DB 998 VCKRKS-----CTPPDPVNGVHVITDIOVSRINYSTCTGHRLLGHSSACCTLS 1048
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QY 2307 P-----VTC-----PDVSSIS-----VEHGRMLIFETOYQOALMLICD 2342
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 QY 2343 PGYYTGTQVIRICQANGKWSLSDSTPTCRIISC---GELPIEPNGHRIQTLV-YGATA 2397
 DB 1228 PGYDLRGAASLHCTPQDWS--PEAPRCVAKSCDDPLQGL---PHGRVFLPILNLQIGAKY 1282
 QY 2398 IFSCNSGTYLVGSRRPRECMANG---LMSGSEVRCLAGHCTGTEPIYVNHINE--NYCY 2451
 DB 1283 SFVCEGFRLLKSSVSHCVLVMRSLMNNVSEVCEHIFCPNPALLNGHTGPPSDIDY 1342
 QY 2452 RGSVYQCN-----AGFRLIMSVRICOQDHH-----WSGKTPFC-VPIYTCG----- 2493
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 QY 2494 ---PENPVNGLTQGNQFNLNDVVKFVCPNGYMBAGARSQCLASQWSDMLPTCRIINC 2549
 DB 1403 PRASPPIPINDE---EPFVGTSLNYECRPGYFGKWFIS-CLLENLWMSVEDNCRKSC 1457
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 DB 1458 GPPPEPFNGMWHIND---TQFSTVNSYSCNEGFRLLGSPFTCLVSGNNVWTDKKA 1513
 QY 2607 CLLVSCGHPSPPHSQMSGDSYT-----VGAVVRYS-----IGKRTLVGN 2647
 DB 1514 CEIISC---EPPTISNDPFYSNNRITSFHNCTVTVYQCHGTPDGEQLFELVGERSTY-- 1567
 QY 2648 STRMCGLDGHTGSLPHCSGISVGVCGDPIPAHGIRLADS---FDPGTVMRPSCEAHV 2704
 DB 1568 CTSKDQYGVWSSPPRCISTN--KCTAPEV-ENAIRVPGNKSFFSLTBIIIRFCOPGFV 1624
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 QY 2763 VATGLSRHCSVNGTWSDEPCLVINGD--PGIPIANGRLGDNFRVKNKTYTQCVPY 2820
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 QY 2922 RGFYSV---RSSVFSCHPEPLVYVSPRRFCOSDGTWSGTOPSCIDPTLTTCADPGVPOG 2978
 DB 1862 GHVLSLYLPMTISYCDPEYLLVGKFICTDQGLMSQLDHYCKE---VNCSPF-LFMNG 1917
 QY 2979 IONN---SOGYQVGSVTLFRCKGYLLOGSTTRTCLPMLTWGCTPP 3021
 DB 1918 IKELDKKVVHYHGYVTLKCEDGYTLRGSFWSQOADDNRD--BP 1961
 RESULT 8
 5256642-10
 ; Patent No. 5256642
 ; APPLICANT: FEARON, DOUGLAS T.; KLICKSTEIN, LLOYD B.; WONG,
 ; WINTIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; IP, STEPHEN
 ; H.; MAKRIDES, SAVVAS; MARSH, HENRY C.; JR.
 ; TITLE OF INVENTION: COMPOSITIONS OF SOLUBLE COMPLEMENT
 ; RECEPTOR 1 (CRI) AND A THROMBOLYTIC AGENT, AND THE METHODS OF
 ; USE THEREOF
 ; NUMBER OF SEQUENCES: 30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/568,128
 ; FILING DATE: 24-SEP-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 412,745
 ; FILING DATE: 26-SEP-1989

APPLICATION NUMBER: 332, 865
 FILING DATE: 03-APR-1989
 APPLICATION NUMBER: 176, 532
 FILING DATE: 01-APR-1988
 SEQ ID NO: 10
 LENGTH: 1847
 556642-10

Query Match 7.5%; Score 1267.5; DB 6; Length 1847;
 Best Local Similarity 21.7%; Pred. No. 7.6e-89;
 Matches 503; Conservative 253; Mismatches 768; Indels 795; Gaps 103;

798 CEEBEVA---YSIRKLOFGVGDITLTFSCPPGYRLGSTARITC-LGRRRLMSSPLPRC 853
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 854 -VAECGSVTGTCTLLSPNFPVNNNNHCTIYSIQTPCKGIOLKAPAFELSGDVLC 912
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 219 YCTSNDOQ--VGWSPAPOCIIPN-----KCTP 245
 973 PGTPEFYKYHDEGHF--AGSSVFSQCDPGYSLRSEELCLSGERRTMDPLPTCYAEC 1030
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 303 -----OPPP-----DVLH----- 310
 1091 PVESGVLLKELSGPALPKDLHSTFNSVLFQSTDFTSKQGFALQFSVSTATSCNDGIP 1150
 311 -----A 311
 1151 QNGSRGSDWEAGDSTVFOCDPGYALQSAEISCVKIEFNFPQSPPTCIAPCGDLTG 1210
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 1211 P--SGVILSPNYEPFPYPPGKCDMKVTSPEYVIALVFNIFLEPGYDFLHIYDGRDLS 1268
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 1324 KNGTRVSDLEKL--GSSVTYYCH-----GVEVEGTSTLCLGPGKRVNNNPPVC 1374
 433 PNGRHTKPLEVFPFGKAVNTTCDPHDRGTSFPLIGESTIRCTSDPGNGVSSPARC 492
 1375 TAPCGGYVSGDVILSPNYPNYNTSGOICLFYTVPEKDYVVFQFAFHITALDVVEH 1434
 493 -----GIL----- 495
 1435 DGHSQ--HSRLLSLSGSHGCESLPLATSNQVLIKFSAGLAPARGF-----HFVQAV 1486
 496 -GHQADHFLFAKLKTQTNASDPFGTS-----LKYCRPEYGRPSITCLDLWVSS- 549
 1487 PR--TSATQSSVPEPRYK--RLGSDFSVGAIVAFECNSGALQSGPEIECLPVGALAQ 1543
 550 PKOVCKRKSCKTPDPNMGVHVTIDIQVSRINYSCTTGHRLIGHSSACCI--LSGNAH 608
 1544 MNVASPTCV--VPCGNLTERRGTLSPGFPEPYLNSLNCWKIIVPBGAGIQIOVASFV 1602
 609 WSTKRPICORIPCGLPRTIANGDFISTNRENFHYS-----VVTYRC 650
 1603 EQMNDLSLEVDPGANITYMLGSPGCTIVPALNNTSQYLHFFSDISVSAAGHLEYKT 1662
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 1663 VGLSSCPPEP--AVPS-----NGVKTGER--YLNDVVSFQCEPFGVALQGHATISCM 1709

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 1770 LNFSTENHDYIELRNGPYETSRMGRFSGSBLPSSLSLSTHETTYFHSQSNRPGFK 1829
 753 -----OPPEVVL-----HAEIRP----- 766
 1830 LEVQAVELQECRDEPRANGIVRGAGYNQSVTFECLPGYOLTGHVLTTCOHGTRNMD 1889
 767 -----DKDNF-----SPQGEVYSCPEGYDLRGAASMRCT--PGDWS 802
 1890 HPLPKCEVPCGAGNTSS--NGTYVSPGFPEPSPSSQDCWLITVPYIGHVRLNLSLQTE 1947
 803 PAAPTCGVKSCDDPMGQLNGRVLFP-----VNQLGAKV----- 837
 1948 PSGDFTIMDGPQOTAPRLGVFTSRMAKTVQSSNQVLKFRHDAATGIFAIAPSAYP 2007
 838 --DFVCD-EGFOLKG-----SSASYCVL-----AGNESLWSSVP 869
 2008 LTK---CPPELILPNAEVTEEN--EEFNIGDIVRYRCLP-----GFTLVGNEILTCRL- 2055
 870 VCBGIFCPSPFVIPNGRHTKPLEVFPFGKAVNTTCDPHDRGTSFPLIGESTIRCTSDP 929
 2056 --GTIQAEPGPPICGV--HCPTELLTDSGVILSOSYPSGYPOFQTSMLVVRPDPY 2110
 930 QNGVW---SSPARCGLIGHCOA-----PD- 952
 2111 NISLTVYPLSEKQYDFELFDGSGOSPLLKALSGVSAPLYVTSSNSGYLWSS- DH 2169
 953 -----HFLPAKLTQTNASDPFGITSLKYECRPEYGRPSITCLDNLV--WSPKX 1002
 2170 AYNRKGFKIRYSAPYCSLPPAPLHGFILQGTSTPGGSIHFGNAGRYLVGSHMAISTRH 2229
 1003 VCKRKS-----CTPPDPVNGMVHVTIDIQVSRINYSCTTGHRLIGHSSACILS 1053
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 2307 P-----VTC-----PDVSSIS-----VEHGRWRLIFETQYFOALMLICD 2342
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 2343 PGYTYTGQVRVIRCOANGKWSLGDSTPTCRIISC--GELPIPNHRICTLSV-YGATA 2397
 1233 PGYDLRGAASLHCTPGDWS--PEAPRCAYKSCDDFLGQ---PHGRVLPPLNLQGLAKV 1287
 2398 IFGNSGTYLVGSRYRCMANG--LMSGEVYCLACHCTPREPIVNGHNGE--NYSY 2451
 1288 SPVCDSEFRLKSGSVSHCVLVGKRSLNWNSVPPVCEHIFCNPRAILNGRHTPGSDIPY 1347
 2452 RGSVVYQCN-----AGFRLIGMSVRICQDDH-----WSKTPFC-VPIYTCG----- 2493
 1348 GKXISTYCDHPDRGMFTNLIGESTIRCTSDPHNGVWSSPARCELSVAAGHCKTBEQF 1407
 2494 ----PGNVNGLTQGNOPNLNDVVKFVGNFGYMEGAARSQCLASGQSMPLPTCRIINC 2549
 1408 PFASPTPIINDF-----EPVGTSLNVECRPGYKMFSS--CLENLWSSVEBDCRKS 1462
 2550 TDRGHQENSROYHASBPHRFSGTYSVYCNHGFYLTGPVLSGQDQ--TWDRRPQ 2606
 1463 GPPEPFGNVHINTD---TOFGSTVNVSCNGBFRLIGPSTTCLVSGNNVTDKAP 1518
 2607 CLVSCGHPGSPHSGWSDSYT-----VGAVVRYSC-----IGKRLVGN 2647

Db 1519 CEIISC-----EPPEITISNGDFYSNNRTSFHNGTVVYQCHTGPDEQLFEIVGERISY-- 1572

Qy 2648 STRMCGLDGHWTSGLPHCSGTSVGVCDPGI PAHGRILDS---FDGTMWRPSCCEGHV 2704

Db 1573 CTSDDQGVWSSPPFCISTN--KCTAPEV-ENATVPGRAPFSLTEIRFCQGFV 1629

Qy 2705 LRGSSEPTQANGSWSGSQPECGVISGNGPTPSNAHVFS--DGLVFSSSIYVECREGY 2762

Db 1630 MVGSHTVQCCOTNGRWGPKLPFCRSRV-CQPPREILHGHTLSHQNFSPQGEVFYSCPSY 1688

Qy 2763 YATGLSRHGSVNGTWMTGSDPECLVINCQD--PGIPANGRLGNDPFTYNTVYQCVPGY 2820

Db 1689 DLRAALHCTPQDWSPEAPRCTVKSQDPLGQLPHGRVLLPLNTQLAKAVFVCDGPF 1748

Qy 2821 MMESHVVS--VLSTCKRTWNGTKPVCKALMCKPPLIPNGKVVS---DEMNGSSVTV 2875

Db 1749 RIKRASHVCLAGMK-ALMNNSSVPVCEQIFCPRPPIALNGRHTGTFPGDIPYGEKISTYA 1807

Qy 2876 C-----LEGQLSLPAVFTCEGNSWGTGLPQC 2903

Db 1808 CDTHPDRGWTFFNLIG-BSSIRCTSDPQNGVWSSPAPRC 1845

RESULT 9

5472939-10

Patent No. 5472939

APPLICANT: FEARON, DOUGLAS T.; KLICKSTEIN, LLOYD B.; MONG, MINNIE W.; GASSON, GERALD R.; CONCINO, MICHAEL F.; IP, STEPHEN H.; MAKRIDES, SAVVAS; MARSH, HENRY C. JR.

TITLE OF INVENTION: METHOD OF TREATING COMPLEMENT MEDIATED DISORDERS

NUMBER OF SEQUENCES: 30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/138,825

FILING DATE: 19-OCT-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 588,128

FILING DATE: 24-SEP-1990

APPLICATION NUMBER: 412,745

FILING DATE: 26-SEP-1989

APPLICATION NUMBER: 332,865

FILING DATE: 03-APR-1989

APPLICATION NUMBER: 176,532

FILING DATE: 01-APR-1988

SEQ ID NO:10:

LENGTH: 2006

5472939-10

Query Match 7.5%; Score 1267.5; DB 6; Length 1847;

Best Local Similarity 21.7%; Pred. No. 7.6e-89;

Matches 503; Conservative 253; Mismatches 768; Indels 795; Gaps 103;

Qy 798 CEEPEVPA--VSIRKGLQGVGDTLTFSCFPGRLEGTAATTC-LGRRRLMSSPLRPG 853

Db 109 CRMPPPVNMVAVIKIQF--GSQIKYCTKGRILGSSSATCIISGDTVINDNTPTIC 166

Qy 854 -VAECANSVTGTGLLSPNFVNYNHNECIYISIQTOPKGIQLKARAFELSEGDVLYK 912

Db 167 DRIPCGLPRTITNGDITSTY--RENFHGVSVTVYRCNPSG--GRKVFEL-VGSP-SI 218

Qy 913 YDNNNSARLLGVFSHEMMGVTLNSTSSLMIDFTDAENISKGELAFSSPELIKCD 972

Db 219 YCTSDNQ--VGIMSGPAPQCIIIPN-----KCTP 245

Qy 973 PGTPEKGYKVHDEGHP--AGSSVSFSCDPQYSLRGSEELLCLSGERTVDRPLPTCVAC 1030

Db 246 PNVEN-GILVSDKRLSLNEVEFRQCPYFVWKGRRYKCAQANK--MEPELPSCSRVC 302

Qy 1031 GGTVRGEVSGQVLSPEYPAPEYHNLCIWTTEAAGCTIGLHFLVDETEVDVLRIMWG 1090

Db 303 -----QPP-----DVLT----- 310

Qy 1091 PVSSGVLLKELSGPALPKDLHSTFNSVLIQFTDFTSKQGAIORFSVSTATSCNDPGR 1150

Db 311 -----A 311

Qy 1151 QNGSRSGDWEAGDSTVFQCDPQVALQGSABEISCVKIENRFWQSPPTCIAPCGDLTG 1210

Db 312 ERTORDKDNFSPGOEVEFYSCBPGYDLRGAASMRCTPQGD--WSPAPACEVASCDDFMG 368

Qy 1211 P--SGVILSPNYPPEYRPPCKEDMKVTSRDVIALVFNIENLEPVDLHIYDGDLSLS 1268

Db 369 QLLNGRVLP-----VNLQAKVDVCD----- 392

Qy 1269 PLIGSEYQQLPGRLESSENLSFLA-----FRSDASVSNAGFVIDYTENPSCFPGSI 1323

Db 393 -----EGFQLKG--SSASVCYLAGMESLWMSVPCVQIF-----CPSPVYI 432

Qy 1324 KNGTRVGSULK-----GSSVTTYCH-----GGVEVEGTSSTLCILGPDCKPVMNNRPVC 1374

Db 433 PNGRHTGKLEVPFPGKAVNYTCDHPDRGTSFDLIGESTICTSDPQNGVWSSPAPRC 492

Qy 1375 TAPCGQVYVGSQVVLSPVYPNYTSQICLYFVTVVPDYVVGQPAFPHALNDVVEVH 1434

Db 493 -----GIL----- 495

Qy 1435 DGHSG--HSRLLSLSGSHTGESLPLATSNQVLIKFSAGLAPARGF-----HFVYQAV 1486

Db 496 -GHQAPDHFLLPAKLTQTNASDPIGTS--LKYECPEYVYGRPFSTICLDNLVWS- 549

Qy 1487 PR--TSATQSSVPEPRYRK-RLGSDFSVGAIVRECNAGVYALQSPREICLPVGAALQ 1543

Db 550 PVDVCKRKSCKTPPDPVNGMVAVITDIOVSINISCTTGHLISHSAECI-LSGNAAH 608

Qy 1544 MNVSAPTCV-VPCCGNLTERGTLSPGPPEBYLNSCWKIVPEGAGIQIVVSPVT 1602

Db 609 WETKRPICQRIKPCGLPPIIANDPISITRENHYS-----VITYNC 650

Qy 1603 EONMDSLEYFGADNTVTMLSGFSGTTVPALINSTNOLYHAFYSDISVSAAGFHEKXT 1662

Db 651 NPGSGGRKVF-----LVGEPS-----LYCTSDN-----DQ 676

Qy 1663 VGLSCPEP--AVPS-----NGVKTGER--YLVNDVYFQCEPGVALQGHANISGM 1709

Db 677 VGIWGPAPQCIIPKCTPPNVENGLIVSDNLSLEAVEFRQCPGKRRVVKQ 736

Qy 1710 PGTVRWVYPPPLCIAQCGGVEEMEGVILSPGFPGNVPNMDCMKIALPVFGAHIQF 1769

Db 737 -ALNMKEBELPSCGRVC----- 752

Qy 1770 LNFSTPEPHDYIEIRNGPEYETSRMMGRPSSELPSSLSTSHETTVYFHSQNRPGFK 1829

Db 753 -----QPPPDV-----HAERTQ----- 766

Qy 1830 LEQAVLEQECDDPEPFANGIVRGAVVNGSVTFECLPGYOLTHPVLVTOCHGNRMWD 1889

Db 767 -----DKDNF-----SPGOEVEFYSCBPGYDLRGAASMRCT--DQDWS 802

Qy 1890 HPLPKCEVPCGNITTS--NGTVVSPGPPSPYSSQDCWMLITVPIGHVRLNLSLQTE 1947

Db 803 PAAPFCEVKSQDDFMQGLNGRVLP-----VNLQAKV----- 837

Qy 1948 PSGDPTITWDPOQAPRLGVFTSMMAKTVQSSNOVLKPHRDATGCIFAIFASVY 2007

Db 838 --DFVCD-EGFQLKG-----SSASVCVL-----AGMESLWNSVVP 869

Qy 2008 LTK--CPPTLPFAEAVVTEN-BEENIGDIYVRCLP-----GFTLVGBELTKL-- 2055

Db 870 VCEQIFCSFVYIPNGRHTGKPLEVFPFGKAVNTTCDHPDRGTSFDLIGSTICTSDP 929

Qy 2056 ---GTYLQFEGPPICEV--HCPTEBLTDSGVILSQSYPSGYPOFOTCSMLVVRBDY 2110

Db 920 QNGVW---SSPAPRCGILGHQA-----PD- 952

Qy 2111 NISLVEYFLSEKQYDEFIFDQPSGQSPLLKALSAGYSAFLITYSSNSYLLMWS--DH 2169

Db 953 -----HFLAKLTQTNASDPFGTSLKVECPREYGRPFSTCLDNLV--WSSPKD 1002
 Qy 2170 AYNRKGRKIVSAPYGLPAPLHGLTSTPGSIFHGCNAGRLVGHSMALCTRH 2229
 Db 1003 VCKRKS-----CTPPDPVNGVHVITDIQVGRINVSCTTGHRLIGHSSAECILS 1053
 Qy 2230 POGVHLWSEALPLCOALSCGLPEAPKNGMFG--KEYVTGTRKAVYSCSEGYH---LOA 2282
 Db 1054 GNTAH-WSTKPRICQRIPCGLPPIANGDFISTNRENFHYGSVVTYACNLGSRGRKVFEL 1112
 Qy 2283 GAETAECL---DTGLMS-----NRNVP-----OCV 2306
 Db 1113 VGEBSIYCTSDNDQVIGMSGAPQCII PNKCTPPNVEGILVSDNRLFLSINEVVDPRCQ 1172
 Qy 2307 P-----VTC-----PDVSSIS-----VHGKRLIFETQYQFOQALMID 2342
 Db 1173 PGFVMKPRRYKCOALNKMBEPLPSCSRVCOPPELIGHGHTPSHONFSPGOEVFYSCE 1232
 Qy 2343 PGVYVTQVYIRCOANGKMSLGDSTPCRIISC---GELPIPNGHRIGHTLAV-YGATA 2397
 Db 1233 PGIDLKGAASLHCTPGQDMS--PEAPRCAYKSCDDFLGOL--PHGRVLPPLNLQLGAKV 1287
 Qy 2398 IFSCNSGYTLVGSRVRECMANG--LWGSSEVRCLAGHCGTPEPIVNGHNGE---NYSY 2451
 Db 1288 SFVCDSEFRLKGSVSHCVLGMKSLMNNVSPVCEHIFCNPRAILNGHGTGTPSGDIPY 1347
 Qy 2452 RGSVYVOCN-----AGRLIGMSVRIICQDDH---WSGKTPPC-VPTICG----- 2493
 Db 1348 GKEISYCDHPDRGMFTNLIGESTRICTSPHNGVWSSPAPRCESLVAGHKRPEQF 1407
 Qy 2494 -----PGAPVNGLTQGNFNLNDVYKFCVCPGYMAEAGARSQCLASGQMDLPTCRILNC 2549
 Db 1408 PPSFTPIPIINDF--EPVGTSLNYECRCREYFGKMSIS-CLENLWSSVEDNCRKXSC 1462
 Qy 2550 TDPGHQENSROYVHASGPHRFSPCTIVSYRCNMGFYLLGTPVLSQCGDG--TWDRBRPQ 2606
 Db 1463 GPPEPFGNGVHINTD---TQFSTVNYSCNEGFRLIGSPSTCLVSGNNVTMDKAPL 1518
 Qy 2607 CLVSCGHPSGSPHSQMSGDSYT-----VGAVVRYSC-----IGKRTLVGN 2647
 Db 1519 CEIISC---EPPTLISNGFYSNMRTSFHNGVTVTQCHTGPDEQLFELVGRSITY-- 1572
 Qy 2648 STMGCLDGHMTSLPHCSGSGVGVCGDPGIPAHGIRLDS---FDBGTWRFSCAGHV 2704
 Db 1573 CTSCDDQVWWSPPRCISTN--KCTAPRY-ENAIWPGNRFSFSLTEIIRFCQGFV 1629
 Qy 2705 LRGSSERTCOANGSWSGOPECVISCNPQTPSNARVFS--DGLVFSSSIYECREGY 2762
 Db 1630 MVGSHTVQCTQNGMGRKLPKCSRV-CQPPPELIGHGHTLSHONFSPGOEVFYSCEPSY 1688
 Qy 2763 YATGLLSRHSVNGTWTGSDECLVINGD--PEIPANGRLGNDPFRYKTVTYQCVPGY 2820
 Db 1689 DLGGAALHCTPGQDMSPEAPRCVKSDDFLGOLPHGRVLLPPLNLQLGAKVSFVCEGF 1748
 Qy 2821 MMESHRS--VLSTKRTNNGTKPVCKALMKCRPPLIPNGKXVS---DFMWSSTIYA 2875
 Db 1749 RLKGRASHCVLWAKM-ALNMSSVAVCEQIFCENPRAILNGRHTGTGPIPYKETSIVA 1807
 Qy 2876 C-----LEGYQLSLPAVPTCEGNGSWTGLPQC 2903
 Db 1808 CDTHPDGKMTFNLIG-ESSIRCTSDPGONGWSSPAPRC 1845

; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/588,128
 ; FILING DATE: 24-SEP-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 412,745
 ; FILING DATE: 26-SEP-1989
 ; APPLICATION NUMBER: 332,865
 ; FILING DATE: 03-APR-1989
 ; APPLICATION NUMBER: 176,532
 ; FILING DATE: 01-APR-1988
 ; SEQ ID NO: 6
 ; LENGTH: 1466
 5256642-6
 Query Match 6.7%; Score 1133; DB 6; Length 1466;
 Best Local Similarity 23.4%; Pred. No. 1,6e-78;
 Matches 402; Conservative 197; Mismatches 620; Indels 498; Gaps 77;
 Qy 1494 CSSVPEPRYK-PLGSDPSVGAIVRECNAGVALQSGPBIETCLVPFGALQAMNVSAPTCV 1552
 Db 52 CKTPDPVNGVHVITDIQVGRINVSCTTGHRLIGHSSAECT-LSGNAHMKSTKPIQC 110
 Qy 1553 -VPQGNLTERRGTILSPGPEBYLNSLNCWKIWPBAGIQTQVVSFVTEQNMDSLEY 1611
 Db 111 RIFQGLPPIANGDFISTNRENFHYGS-----VVTYRCNPGSGGRKV 152
 Qy 1612 FDGADNTVTLMSFSGSTTVALLNSTSNQLYLHFYSDISVSAAGFHELYTVGLSCPEP 1671
 Db 153 FE-----LVGSPS-----LYCTSND-----DOVGIWSPAP 178
 Qy 1672 --AVPS-----NGVKTER---YLNDVVSFOCEPGYALOOHAHISCMPTVRMNY 1718
 Db 179 QCIIPKCTPPNVEGILVSDNLSFLSINEVERCOPGVGMKPRRYKQ--ALNKMP 236
 Qy 1719 PPLICAOCCGTVEMEGVILSBPGFNGYPSNMDCKWIALPVGFAHIOFLNFSTEPNH 1778
 Db 237 ELPSCSRVC-----QPP 249
 Qy 1779 DYIERNGPYETSRMGRFSGELPSLSLSTSHETTYFHSDSQNRPGFKLEYQAYELO 1838
 Db 250 DVL-----HAERTOR----- 259
 Qy 1839 ECPDPEPFANGIVRGAGVNVGOSTFECPLPGYOLTGHPVLTQCHTRNMDHPLPKCEVP 1898
 Db 260 ---DKDNF-----SGQEVFYSCEGYDLKGAASRCT--PGQDMSPAAPTEBVK 304
 Qy 1899 CGGNITSS--NGTVYSPGFPSPYSSSQDCVWMLTVPVIGHVRLNLSLQTEPQDFTTIW 1956
 Db 305 SCDDFMQQLNGRVLP-----VNLQLGAKV-----DFVCD- 335
 Qy 1957 DGPQCTAPRLGVFTSRMAKTTVOSSNQVLKTHRDAATGCIAPALASAVPLTK--CPR 2013
 Db 336 EGFQLKQ-----SSASYCVL-----AGMSLWMSVAVCEQILCPFS 371
 Qy 2014 PTLIPNAEVATEN-EEFNIGDIYRCLP-----GFTLVGNELTQCL-----GTLYQF 2061
 Db 372 PVPVPMNRHTGKPLEVFPFKAVVNYTDDPHPDGTSFDLIGESTIRCTSPQNGVW-- 428
 Qy 2062 EGPPLICEV--HCPTELLTDSGTGVLISQSPGSPQFOTCSMLVRVEPDPYNI SLVEYF 2119
 Db 429 SSPAPRGILGHQA-----PD-----HF 447
 Qy 2120 LSEKQYDEFEIFDPSGQSPFLKALSGNYSAPLIVTSSNSVYLRMS-DHAYNRKGFKI 2178
 Db 448 LFAKLKTQTNASDPFGTSLKVECPREYGRPFSTCLDNLV--WSSPDVCKRKS--- 501
 Qy 2179 RYASAPYSLRAPLHGLTSTPGSIFHGCNAGRLVGHSMALCTRHPOGYHLMSE 2238
 Db 502 -----CTPPDPVNGVHVITDIQVGRINVSCTTGHRLIGHSSAECILSNTAH-WST 554
 Qy 2239 APLCOALSCGLPEAPKNGMFG--KEYVTGTRKAVYSCSEGYH---LOAGAETAECL 2291
 Db 555 KPPICQRIPCGLPPIANGDFISTNRENFHYGSVVTYRCNLGSRGRKVFELVGPSTYCT 614

RESULT 10
 5256642-6
 ; Patent No. 5256642
 ; APPLICANT: PEARON, DOUGLAS T.; KLICKSTEIN, LLOYD B.; WONG,
 ; MINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; IP, STEPHEN
 ; H.; MAKRES, SAVVAS; MARSH, HENRY C. JR.
 ; TITLE OF INVENTION: COMPOSITIONS OF SOLUBLE COMPLEMENT
 ; RECEPTOR 1 (CR1) AND A THROMBOTIC AGENT, AND THE METHODS OF
 ; USE THEREOF
 ; NUMBER OF SEQUENCES: 30

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QY 2292 ----DTGLMS-----NRNVP-----QCV-----2307
DB 615 SNDDVGATWSGAPPOCIIPNKCTPBNVNGILVSNRSLFSLNEVERECPGVMKGR 674
QY 2308 -VTC-----PDVSI-----VHGMRLLFETQYFOQALMLICDPGYTGTOR 2351
DB 675 RYKCALNKMBELSCSRVCPPEILHGHENTPSQNFSGQVFYSCPGYDLGAA 734
QY 2352 VTRCOANGKSLGSDTPTCRILISC-----GELIPBNHRIGHTLAV-YATALIFGNGSYT 2406
DB 735 SLHCTPRDMS--PAPRCAYKSCDDFLGOL--PHGRVLPMLDQCAKVSFVCDGFR 789
QY 2407 LVGSFVRECMANG--LWSGEVRLACHGTPETVINGHNGE--NYSYRGSVYQCN 2460
DB 790 LKGSVSHCVLWGMKSLWNNSVPCENHFCNPPAILNGRHTGTPSGDIPRGKISTCD 849
QY 2461 -----AGFRLIGMSVRICODH-----WSGKTPRC-VPTTCG-----PSNPV 2498
DB 850 PHPRGMTFNLIGESTTRCTSDPHGNGVWSSPAPRCESLVRAHCKTPEOPFPFASPTIPI 909
QY 2499 NGLTQGNQFNLDVVKFVCPNGYMAEGARSOCLASGQMSDMLPTCRILINCTDGHQENS 2558
DB 910 NDF-----EFVGTSLNTECRBGYFGKMSIS-CLBNLWSSVEENDCKRKSOGPPPPNG 964
QY 2559 VROVHASGPPHRSFGTIVSYRCHGFYLLGTPLVLSQGDG--TWDRPPOCLLVSCGHP 2615
DB 965 MVHINTD---TOGSTVYVSCNCGFRLIGSPYTTCLVSGNNVTWMDKAPICELISC--- 1017
QY 2616 GSPHSQMSGDSY-----VGAVVYVSC-----IGKRTLGNSTRMCLD 2656
DB 1018 -EPPITISNGDFYNNKRTSFNGTAVTYOCHTGDGOLFELVGERISY--CTSKDOVQ 1074
QY 2657 HMTGSLPHCSGTAVGCGDGPPIPAHGIRLGS--FDPGTVMRFSCEAGHVLGSSERTC 2713
DB 1075 VMSGPPRCISTN--KCTAPEV--ENALRVGNRFFSLTEIIRROQPGVVMGSHTVQC 1131
QY 2714 QANSGMSGQPECCVIVCGNPGTSMARVVS--DGLVFSISVYECREBYATGLLSRH 2771
DB 1132 QTNRMWPKLPKHCGRV--QPPPEILHGHNTLSHODNPSQGEVYFSGEPDYDRGAASH 1190
QY 2772 CSVNGTGTGSDPECLVINCDD--PGIPANGRLGNDPRYKTYVOCVPYMMESHRSV- 2828
DB 1191 CTGPGDMSPEAPRCTVASCDDFLGOLPHGRVLPMLDQCAKVSFVCDGFRIGKSASH 1250
QY 2829 -VLSCTDRTWNGTKVYCKALMKCPPLINGKAVGS--DFWMSGVYAC-----2876
DB 1251 CVLAGMK-ALMNSGVPCQEIFCPNPPAILNGRHTGTPFGDIPYKEISYACOTHPDRGA 1309
QY 2877 ---LEGVQLSLPAVFTCEGNSWTGELPOC--FPVFCGDPGVPSRGREDRGFSY--R 2927
DB 1310 TPNLIG-ESSIRCTSDPDQNGVWSSPAPRCESLVPAACPHPKIQNGHYIGHVSLSYLRG 1368
QY 2928 SSVFSCHPPLVIVGSPRRFCOSDGTWGTGTPSCIDPTLTTCADPGVPFGIOWN--SO 2984
DB 1369 MTSYCTCDPGYLLVVGKGFICTDQGISQDLHCKE--VNGSFP-LFMNGISKELEMK 1424
QY 2985 GYGVGSTVLFRCQKGYLLQSGTTRTCLPMLTSGTTP 3021
DB 1425 VHYHYGVTLKCEDGYTLGSPMSQCADRWD--PP 1459

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FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 588,128
FILING DATE: 24-SEP-1990
APPLICATION NUMBER: 412,745
FILING DATE: 26-SEP-1989
APPLICATION NUMBER: 332,865
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APPLICATION NUMBER: 176,532
FILING DATE: 01-APR-1988
SEQ ID NO: 6
LENGTH: 1466
5472939-6
Query Match 6.7%; Score 1133; DB 6; Length 1466;
Best Local Similarity 23.4%; Pred. No. 1.6e-78;
Matches 402; Conservative 197; Mismatches 620; Indels 498; Gaps 77;

QY 1494 CSVPEPRYCK-RLGSDFSVGAIVRPECNSGVALGSPREIECLPVGALAOHNVNAPTCV 1552
DB 52 CKTPDPVUNGMVHVITDIOVGRINYSCTTGHRLIGHSSAECT-LSGNAAHMSTKPPICQ 110
QY 1553 -VPCGNLTERGTLISPGFPPYLYNSLNCWKIVPEGAGIQIOVSVFTEQNMDSLEV 1611
DB 111 RIFCGLPPTIANGDFISTRENPHYGS-----VVTYRCRPSGGRKV 152
QY 1612 FPGANDTYMGLSPGCTIVPALNSTSNQULHFFYSDISVSAAGFHLBYKTVGLSSCEP 1671
DB 153 FE-----LVGEPs-----IYCTSDND-----DOYIGWGPAP 178
QY 1672 -AVPS-----NGVATGER--YLNDVVSFOCEPBGVALOGHAH:SCMPGTVRANRY 1718
DB 179 QCIIPKCTPRVENVGILVSDNRSLFSLNEVERECPGQFVWKGRRVKCO--ALNKWEP 236
QY 1719 PPLCLAOCCGTVEBMEGVILSPGPPGYPSNMDCMKIALPVGGAHIOFLNFSTERNH 1778
DB 237 ELPSCSRVC-----249
QY 1779 DYIEIRNGPYETSRMGRFSGSELBSLSLSTSHETTYVPHSDHSONRPFKLYOAYELQ 1838
DB 250 DVL-----HAEKTR-----259
QY 1839 ECPDPEPANGIVRGAGYVNGQSVTFECLPGYOLTGHPVLTCOHTNRMNDHPLKCEVP 1898
DB 260 ---DKDNF-----SPQGEVYFSGEPDYDRGAASHMCT--POGDWSPAPPTCEVK 304
QY 1899 CGGNTSS--NGTYVSRFPSPYSSQDCWLVITVPYGHGVRALMSLQTEPSEGDFITW 1956
DB 305 SCDDMGQLNGRVLFP-----VNLQCAKV-----DFVCD- 335
QY 1957 DGPOQTARLGVFTRSMAKKTVOSSNQVLKPFHRDATGIFALAFSAVPLTK---CP 2013
DB 336 EGFOLKG-----SSASYCVL-----AGMESLMNSVPCQIIFCS 371
QY 2014 PTLIPNAEVTEEN-EEFNIGDIYRYCLP-----GFTLVGNELLTKL-----GYLQF 2061
DB 372 PPVIPNGRHGKPLEVPPFGKAVNYTCDPHDRGTSFDLIGESTRICTSDPDQNGWV--- 428
QY 2062 EGPPICEV--HCPTELNDLSTGIVILSOSYVPGYPPQFCISMVLRVPPDYNISLTYEYF 2119
DB 429 SSPAPRCGILGHCA-----PD-----HF 447
QY 2120 LSEKQYDEFELFDPSQSPPLKALSGNYSAPLIVTSSNSVYLRWMS-DHAAYRKQFKI 2178
DB 448 LFAKLTQTNASDPPISTLSKYERPRYGRPSITLIDLNV--WSPRDVCKRKS--- 501
QY 2179 RYSAPYCSLPAPLHGTLIQSTIQPGGS:HFQCNAGYRVLVGSMAICTRHPOGYHLMSE 2238
DB 502 -----CKTPDPVUNGMVHVITDIOVGRINYSCTTGHRLIGHSSAECILSGNTAH-WST 554
QY 2239 AIFLQALSGLPEAPKNGWVFG---KEYTVGKAVYSCSEGVH---LQAGNATIECL 2291
DB 555 KPPIQRIPOGLPPTIANGDFISTNENPHYGSVVTYRCNLGSRGRKRVFELVGPSTIYCT 614

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RESULT 11
5472939-6
PATENT NO. 5472939
APPLICANT: FEARON, DOUGLAS T.; KLICKSTEIN, LOYD B.; WONG,
WINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; IP, STEPHEN
H.; MAKRIDES, SAVVAS; MARSH, HENRY C. JR.
TITLE OF INVENTION: METHOD OF TREATING COMPLEMENT
MEDICATED DISORDERS
NUMBER OF SEQUENCES: 30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/138,825

```

QY	2292	----	DTGLMS-----	-NNNVPP-----	-----	QCPR-----	2307
Db	615	SNDQVGV	MSBPAPQCIIPNCKTP	ENWENGLV	SDNLSL	BSLNEV	FRCPGFVMKGR 674
QY	2308	-VTC-----	PDVSSIS-----	-VHGWRMLF	ETQYOFOA	QMLICDPGY	YVTGOR 2351
Db	675	RVKCOALNKMBELP	PSGRCVQCPPEL	IGHHTSHQDN	FSRGGV	FPSCBGR	DLRGA 734
QY	2352	VIRQANGKSLG	STPFCRIISC---	GELPIPN	GRIGTSLV	-YATAI	FGSNGYT 2406
Db	735	SLHCTPRDWS-	-DEAPRC	AVSCDPLF	GOL---	PHGRVL	PELNIQLCAKKS
QY	2407	LVGSRVRECMANG---	LMSGEV	BLACHGCP	PEPIV	YNGHNGE---	-NYSRGS
Db	790	LKGSVSHVCVLV	GRSLMNNV	PRVCEHIF	CENP	PAILNGHRT	GPBGDI
QY	2461	-----	AGFRLIGMS	SVRLCOQD	HH-----	WSGKTPEC	-VPITCGH-----
Db	850	PHDPGRMTFNL	IGSTRICTSD	PHQNGV	SSPAPRC	CELSVBA	GCKTPEGRFP
QY	2499	NGLTQGNFNL	NDVVKFVCNPG	YAAEGAA	BQCLAS	GSQSDMLP	FCRIINCTD
Db	910	NDF-----	EFPGTSL	NEBCRGY	PRKMFIS-	CLENLW	SSVEBDCRKS
QY	2559	VROVHASGPRH	FSFGTITV	SYRNCGFY	LGTPTV	LSQGD---	-TMDRR
Db	965	MVHINTD----	TOGSTV	YSCNBS	FRLIGSB	STTCLV	GSNNVTMDKAP
QY	2616	GSPPHSONSG	SDYT-----	VGA	VVRYSC-----	-IGKRLV	GNSTRMCGLDG 2656
Db	1018	-EPPPTIS	NGDFYSGN	NRTRS	FNHNGV	VVTYQCH	TGHPDGEQL
QY	2657	HWTSGLP	HCSTSV	GCVD	PGCI	PAHG	ITLGS---
Db	1075	VMSSPP	PRCISTN-	KCTAP	BEV-ENAL	IRVPGNR	SFFSLTEIIR
QY	2714	QANSWS	GSQPECCG	VCISG	NPCTP	SNARVFS-	DGLVFSS
Db	1132	QTNRMGR	KXLP	PHCSR	V-CQ	PELIGH	HTLSHQDN
QY	2772	CSVNGT	WTGSD	DECLV	INC	GD-PCIP	ANGLRG
Db	1251	CVLG	GMK-ALW	NSSPVCE	QIFCP	NP	PAILNG
QY	2877	---LEGV	OLSP	PAVTC	GCNGS	MTGEL	QOC---
Db	1310	TFNLI	G-BSS	IRCHSD	PDGNG	WSSBP	ARCELSV
QY	2928	SSVSF	SCHP	LVLV	GSPP	RFCSQ	SDGWS
Db	1369	MTISY	CTD	PGX	LVLV	GKGFIF	CTDQGI
QY	2985	GVOY	GSTVL	FRCCQ	GYL	LGSTTR	CLEPNL
Db	1425	VYH	YDVT	LKCE	DGYTL	EGSSP	WSOCQ
RESULT 12	5256642-5						
1	PATENT NO. 5256642						
2	APPLICANT: FEARON, DOUGLAS T.; KLICKSTEIN, LLOYD B.; WONG, WINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; IP, STEPHEN H.; MAKRIDES, SAVVAS; MARSH, HENRY C. JR.						
3	TITLE OF INVENTION: COMPOSITIONS OF SOLUBLE COMPLEMENT RECEPTOR 1 (CRL) AND A THROMBOLYTIC AGENT, AND THE METHODS OF USE THEREOF						
4	NUMBER OF SEQUENCES: 30						
5	CURRENT APPLICATION DATA:						

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; APPLICATION NUMBER: US/08/588, 128
; FILING DATE: 24-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 412, 745
; FILING DATE: 26-SEP-1989
; APPLICATION NUMBER: 332, 865
; FILING DATE: 03-APR-1989
; APPLICATION NUMBER: 176, 532
; FILING DATE: 01-APR-1988
; SEQ ID NO: 5
; LENGTH: 1537
5256642-5

Query Match      6.7%; Score 1133; DB 6; Length 1537;
Best Local Similarity 23.4%; Pred. No. 1.7e-78;
Matches 402; Conservative 197; Mismatches 620; Indels 498; Gaps 77

1494 CSSVPEPRYK-RKGSDFSVGAIVFECNSGYALQGSBELECLVPGLAQMVSAPTGV 1552
52 CKTPDPDNGMVHVITDIQVGRINSCTTGHRILGHSSACI-LSGMAHMTKPIQ 110
1553 -VPGGNLTERKGTILSBGFPEPLINSNCWKIVPEGAGIQIQQVVSFVTEQMDLSLV 1611
111 RIPGLPPTIANGFELSTNRENFRYGS-----VYTRCNPGSGGRKV 152
1612 FDGADNVTYMLGSPSGTVPALLNSTSNQLYLHFYSDISVSAAGPHLEKTVGLSCREP 1673
153 FE-----LVGEPS-----IYCTSD-----DOVGIWSGAP 178
1672 --AVPS-----NGVKTGER---YLVNDVVSFQCEBVALQGHANISCMPTVRWNY 1718
179 QCIIPNKTPTNVENGLIVSDNRSLFSLNEVFEPRCQGFVWKGBRRVKQ--ALNKWER 236
1719 PPLICIAQCGTVEEMESVILSPGRPGYBNBNMDCMKIALPVFGAIIQIPLNSTERNH 1776
237 ELFPCSRVC-----:
1779 DYIETRNGPYRTSMWGRFSGSELPSLSTSHETTVFHSHSQNRPGFKLEYQAYELQ 1836
250 DVL-----HARRQR-----QPP 249
1839 ECPDPEPANGIVRGAGYNGQSVTECLPGYOLTGHEVLTQHGNTNEMDPLPKCEVP 1896
260 ---DKDNF-----SPGEVFEVSGCEPYDLRGAASMRCT--PGDMSPPAAPTCEVK 304
1899 CGGNITSS--NGTYVSPGFPSPYSSQDCWMLIVPIPIGHGRVRLNLSLQTEPSGDFITW 1955
305 SCDFMFCQQLNIGRVLFP-----VNLQIGAKV-----DFVCD- 335
1957 DGPOQTAPRLGVITRSMAKTVOSSNQVLTKFHRDAATGIPAIAFSAVPLTK--CP 2013
336 EGFQDKG-----SSASVCVL-----AGMESLIMNSVVCBDIFCPDS 371
2014 PTILPNAEVETEN-EEFNIGDIVRYRCLP-----GFTLVGNEILITCKL-----GTYLQF 2061
372 PPIVIPNGHNTKPLEVPPFGKAVNYTCDPHDRGHSFDLIGESTRICTSDPGNGWV-- 428
2062 EGPRIICEV--HCPTNELITDSTGVILISQSPGSAVPQQTQSMVLVREPDVNISLTVEYF 2119
429 SSPAPRCGILGHCA-----PD-----HF 447
2120 LSEKQYDFEFLFDPSGQSPLKLALSGNYSAPLITVSSNSVYLRMS--DHAYNRKGFKI 2178
448 LPAFLKQTQVNSDPPIGTSLKYEGRPEYGNRPSITCDNLV--WSPKPOVCKRKS--- 501
2179 RYSAPYCSLPAPLHGLIGOTSTQPGCSIHFGCNAGRYLVGHSMALITRHPQGYHLMSE 2233
502 -----CKTPDPDNGMVHVITDIQVGRINSCTTGHRILGHSSAECILSGNTAH-WST 554
2239 AIPICQALSGLEPAPRNKGVWFG--KEYTVGTAAVVSCEGHV---LQAGAEATACL 2291
555 KPPIQIRPCCGLPPTIANGDEISTNRREAFHGSVYVYTRCNIGSGRKRKVFELVGEPSITCT 614

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QY 2292 ----DTGLMS-----NRNVPP-----OCVP-----2307
D 615 SDDQVGIWISGPAPQCIIPNKCTEPNVENGILVSDNLSFLSINEVEFRQIPVWVKMPR 674
QY 2308 -VTC-----PDVSSIS-----VEHGRMLIFETQIQFOAQLMLCDPGYYTGOR 2351
D 675 RVKQALNKKPELPSCSRVCQPPPELHSHHTPSHDNPSPGQEVFVSCPEGYDLRGAA 734
QY 2352 VIRCOANGKMSLGDSTPTCRILISC-----GELPIPNNGHRIQTLISV-YGATAIFSCNSGYT 2406
D 735 SLHCTPRGDMSS--PEARCAVKSCDLFLGOL--PHGRVLPPLNQLGALVAFVCDGGR 789
QY 2407 LVSGRVEECMANG--LMSGEVACLAGHCCTEPPIVNGHINEB--NYSRGSVVYQCN 2460
D 790 LKGSVSHCVLVGMRSLMNNNSVPVCEHIFCPNPPALINGHHTGTPSGDIDYGRBISYTC 849
QY 2461 -----AGFRLIGMSVAVICQODNH-----NSGKTPFC-VPTTCGH-----PCNPV 2498
D 850 PHPDGKMTFNLIGSTIRCTSDPHGNGVWSSPARCCLSVRAGHCKTPEQFPASPPIPI 909
QY 2499 NGLTQGNQFNLNDVKKFVCNPGYVMAEGARSQCLASGOWSMDLPTCRILINCTDPGHQENS 2558
D 910 NDF-----EPVUGSLNTECRPGYTGKMFIS-CLENLVWSSVEDNCRKSCGPEPPEFG 964
QY 2559 VROVHASGPHRFSFGTIVSYRCHNFYLLGCTPVLSCQGDG--TWDRPBPQCLLVSCGP 2615
D 965 MHVINTD-----TOFGSTVNYSCNEGFRLLIGSPSTTCLVSGNNVTPDKKAPICELISC-- 1017
QY 2616 GSPHSGMSGDST-----VGAIVRYSC-----IGKRLVGNSTRMGLDG 2656
D 1018 -BEPPTISNDPFSNNNTSFHANGVIVVYQCHTGPBGOLFELVGERISY--CTSKDQVG 1074
QY 2657 HMTGSLPHSCGTSVGVCGDPIPAHGIRLGDSS--FDPGTVMRFSCEAGHVLGSSERTC 2713
D 1075 VMSSPPRCJSTN--KCTABEV-EMARVPGNRSFBLTEIIRFCQPGVVMGSHITVC 1131
QY 2714 QANGSWSGQPECGVISCNPGTPSNARVVS--DGLVFSSSIVYECREGYVATGLLSRH 2771
D 1132 QTNGRMGPKLPHCSRV-CQPPPELHGHHTLSHDNPSPGQEVFVSCPEPYDLRGAAJLH 1190
QY 2772 CSNVGTMGSDPRECLVINGCD--PGIPANGLRLGNDRYKTYTQCVPRYMMSHRVS- 2828
D 1191 CTRQGDSPAPRCVYASCDPLGQDLHGRVLLPLNLQLGAKVSPCDBEFRLKGSASH 1250
QY 2829 -VLCTDRMTNGTKPVCKALMKCPRELLPNGLKVVGS--DFMWSGSVTVAC-----2876
D 1251 CVLAGMK-ALMNSGVPCEQIFCPNPPALINGHHTGTPFGDIYKKEIISTACDTHPDRGM 1309
QY 2877 ---LEGQSLPRAVFTCEGNSWTGELPQC--PVFPCGDPGVPSRGRREDRGFSY--R 2927
D 1310 TFNLIG-ESSIRCTSPDQNGVWSSPARCELSVPAACPHPKIQNGHYIGHVSJLPLG 1368
QY 2928 SSVFSCHPPLVVGSPRRCQSDGTMWGTQPSCIDPULTTCADPGVPOGQIGN--SQ 2984
D 1369 MTSITCDPEYLVVGKFLPCTDQGLMSQLDHYCKE--VNCSPF-LFMNGISKELEMMK 1424
QY 2985 GYGVGSVTLFRCCQGYLLQGSTTRCTLPNLTWSGTP 3021
D 1425 VHYGDVYTLKCGEDYTLBSSPWSQOQADRDMD--FP 1459

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RESULT 13
5472939-5
; Patent No. 5472939
; APPLICANT: FEARON, DOUGLAS T.; KLICKSTEIN, LOYD B.; WONG,
; WINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; IP, STEPHEN
; H.; MAKRIDES, SAVVAS; MARSH, HENRY C. JR.
; TITLE OF INVENTION: METHOD OF TREATING COMPLEMENT
; MEDIATED DISORDERS
; NUMBER OF SEQUENCES: 30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/06/138, 825
; FILING DATE: 19-OCT-1993

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 588, 128
; FILING DATE: 24-SEP-1980
; APPLICATION NUMBER: 412, 745
; FILING DATE: 26-SEP-1989
; APPLICATION NUMBER: 332, 865
; FILING DATE: 03-APR-1989
; APPLICATION NUMBER: 176, 532
; FILING DATE: 01-APR-1988
; SEQ ID NO: 5
; LENGTH: 1537
5472939-5
Query Match 6.7%; Score 1133; DB 6; Length 1537;
Best Local Similarity 23.4%; Pred. No. 1, 7e-78;
Matches 402; Conservative 197; Mismatches 620; Indels 498; Gaps 77;

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QY 1494 CSSVPEPRYK-RLGDSFSGAIVRECNAGYALQSPREICLPVPGALAMNVASAPTCV 1552
D 52 CKTPDPVGVGMHVITDIOVGSRIYVSCCTGRLIGHSSAECI-LSGNAAMHSTKPIQ 110
QY 1553 -VPCGNLTERGTLISPGFPEPYLNSLNCWKIIVPEBAGIQIYVSFVTEQNDLSLV 1611
D 111 RLPCLPPTIANGDFISTNRENPHYGS-----VVTYRCNPGSGGRKV 152
QY 1612 FQADNTVMLGFSQGTIVPALLNSTNQYLHFYSDISVSAAGFLHEKYTGVLASCPBP 1671
D 153 FE-----LVGEPS-----IYCTSDN-----DQVINGSGAP 178
QY 1672 --AVPS-----NGVKTGER--YLVDVVSFOCEPQYALQGHANISCMGTVARMY 1718
D 179 OCILIPKCTPENVENGILVSDNRSJFSLNEVEVFCQPGVWVKGPBRVVCQ--ALNKKWP 236
QY 1719 PREPLCAOCCGVEMEGLVILSPGFPGVPSMDCSKIALVVGCAHQLFLNSTERPH 1778
D 237 ELRPSGRVC-----QBP 249
QY 1779 DYIEIRNGEYETSRMNGRFGSGELPSLSLSTSHETTVVPHSDSQNRPGFKLEYQAYELQ 1838
D 250 DVL-----HARTOR-----QBP 259
QY 1839 ECPDPEPPANGIVRAGVNGSVTFECLPGYQLTGHVPLTQCHGTNRNMDHPLPKCEVP 1898
D 260 ---DKDNF-----SPQGEVYFVSCPEGYDLGAAISMRT--PQGWSSPAAPCEVVK 304
QY 1899 CGGNITSS--NGTVSPGSPSPSYSSQDCVMILITPIGIGVYLNLSLQTESGDPITW 1956
D 305 SCDDFMGOLLNGRVLFP-----VNLQLGAKV-----DPCD- 335
QY 1957 DGPQOTAPRLGVFTSMMAKKTVOSSSNQVLLKFRHDAATGIFAIFASAYPLTK---CP 2013
D 336 EGFOLKG-----SSASYCVL-----AGMSLMSNSVPCQIFCFS 371
QY 2014 PTLTNAEAVTEN-EEFNIGDIVRYCLP-----GFTLVGNELITCKL-----GTLYOF 2061
D 372 PVIINGHHTGKPLRLEVFPFGKAVNYTCDBHPDRGTSFLLIGSTIRCTSDPGNGVW--- 428
QY 2062 BGPPIICEV--HCPINELLTSTGVILSOSYDGSIPQOTCSMLVREPDNVIISLVEYF 2119
D 429 SSPAPRCGLIGHCQA-----PD-----HF 447
QY 2120 ISEKQYDEFELIPDGSQSPLLKALSGVNSAPLIVTSSNSVYLLMSS-DHAYNRKGFKI 2178
D 448 LFAKTKGTQNASDFIIGTSLKKECPREYGRFSTICDNLV---WSPKVDYCKRS--- 501
QY 2179 RYSAPYCSLPRAHLGHFLIGTSTQPGSIHFGCNAGYRLVGHNSAICTRHPQGYHLMSE 2238
D 502 -----CKTPDPVGVGMHVITDIOVGSRIYVSCCTGRLIGHSSAECILSGNTAH-WST 554
QY 2239 AIPLOALSCGLPEAPKGMVFG---KEYTGTAKVYSCSBEYH---LQAGAEATBEL 2291
D 555 KPPICORIPCGLPPTIANGDFISTNRENPHYGSVVTYRCNLSGRKRVFELVGEPSIYCT 614

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QY 2292 -----DTGLMS-----NRNVPP-----OCVP----- 2307
DB 615 SNDQVIMSGPARQCIIPNKCTPNNVENGILVSDNLSLFSNLVEFRQCPGVKMPR 674
QY 2308 -VTC-----PDVSSIS-----VEHGMRLIFETQVQFOALMLCDPGYYTGOR 2351
DB 675 RVKQALNKMEPELPSRVCQPPPEILHGHNTSHODNFSPQGEVFSCEPGYDLGAA 734
QY 2352 VIRCQANGKXSLGSTPTCRISC-----GELPIPNHRICTLSV-XGATAFSCNSGYT 2406
DB 735 SLHCTPRGDSW--PEARCAVAKSCDDFLGOL--PHGRVLFPLNLQLGAKVSFYCDECFR 789
QY 2407 LVGSRYRECMANG--LMSGEVRLAGHCTPEPIYVNGHNGE--NYSYRGSVAVQCN 2460
DB 790 LKSSSVSHCVLVGKRSILMNSVPVCEHIFCPENPAILNGHRTGPSGDIYFKKISITCD 849
QY 2461 -----AGFRILGMSVRIQQODHH-----WSGKTPFC-VPIITCGH-----PGNPV 2498
DB 850 PHPRGWTFLIGESTIRCTSDPHNGVWSSPAPRCELSVAGHCKTPEQEPFASPTIPI 909
QY 2499 NGLTQGNQFNLNDVYKRVCPNGYMAEGAASQCLASQMSDMLPTCIIINCTDGHQENS 2558
DB 910 NDF-----EPVGTSLNECRPPGYGKMFIS-CLENLWSSVEDNCRKSCGPPPEPFG 964
QY 2559 VROVHAGPFRFSFGTTVYRCNHGFYLGTPVLSCQGDG--TWDRPPQCLLVSCGHP 2615
DB 965 MWHINTD--TQGSTVNVYSCNMGFRILIGSPITCLVSGNNVTWDKAPICELIISC-- 1017
QY 2616 GSPHSGMSGDSYT-----VGAIVRYSC-----IGKRTLVGNSTRMCGIDG 2656
DB 1018 -BPPPTISNGDFYSNNRTSFFNGTVVTVYQCHTGPDSQLFELVGERSIY--CTSKDQVG 1074
QY 2657 HMYGSLPHGCGTSVGVCGDEIPAHGIRLQDS--PFGTYMRSSCEAGHYLRSSERTC 2713
DB 1075 VMSSPPRCISTN--KCTABEV-ENAIKVPQNRSPFLTELIRRCOPGFVMVGSHTVOC 1131
QY 2714 QANGSMGSGQPECCVISCNPGTPSNARVVS--DGLVSSSIYECREGVYAGLLSRH 2771
DB 1132 QTNKRWKPKLPHGCRV-CQPPPEILHGHNTSHODNNSPQGEVYSEPEYDLGAA SLH 1190
QY 2772 CSVNGTGTGSDPECLVINGCD--PGIPANGRLANDFRYKNTVTVYQCPVGMESHRSV- 2828
DB 1191 CTPOGDMSPAPRCTVASCDFLQGLPHGRVILPLNLQLGAKVSFYCDEGRFLKGRASH 1250
QY 2829 -VUSCTDRTWNGKRPCKALMKCPPLIPNGKTVGS--DFMNGSSVTAAC----- 2876
DB 1251 CVLAGMK-ALMNSSVPVCEQIFCENPAILNGHRTGTPFGDIPYKKSISVACDTHPDRGM 1309
QY 2877 ---LEGVQLSLPAVFTCEGNGSWTGLPQC--FPVFCGDRGVPSRGRREDGRFSY--R 2927
DB 1310 TPNLIG-ESSIRCTSDPOGNGWSSPAPRCELSVPAACPHPKIQNGHYIGGHVSLVLP 1368
QY 2928 SSVSFSCHPPLVIVGSPRRFCQSDGTWSTGTOPSCIDPILTTTCADPGVPOFGIONN--SQ 2984
DB 1369 MTISYCTDPGLVVGKGFIFCTODGIVSQIDHYCKE--VNCSPF-LFMNGISLELMK 1424
QY 2985 GYGVGSYTVLPRCQKGYLLOGSTTRTCLPMLTWSGTTP 3021
DB 1425 VHYGDVYTLKCEBDGYTLBGS PWSQCOADDRMD--PP 1459

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; PRIOR APPLICATION NUMBER: 60/111873
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: 60/080550
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1012
; TYPE: PR
; ORGANISM: mouse
US-09-285-385C-4

Query Match
Best Local Similarity 22.9%; Pred. No. 1,4e-50;
Matches 290; Conservative 170; Mismatches 417; Indels 392; Gaps 48;

QY 1022 PLPTVAECGGTYRGEVSGVLSPGYAPAYEHNLNCITWTIEAGCTTGHFLVFTDEEV 1081
DB 17 PLDR-----GAVTGDHNSVALDYG-----ALEGEGTBOQLHY----- 50
QY 1082 HDVLRITWDGVEBSGVLLKELSGPALPKDHLSTNSVVLQFSTDFTSKQGFALQFSVSTA 1141
DB 51 HD-----PCKAVFWGDI--ALDEDDLKLFH--IDKAEWM-----TK 83
QY 1142 TSCNDPG-----IPNGSRSGDSWEAGDSTVPOCDPG--YALQSGAE 1181
DB 84 PSIDKPHDPTGCLSETSARPNDTASNASIQARKKQDKATTLPLNPGTSNTAKTTSAR 143
QY 1182 I-SCVKIENPFQPSBPPTCIAP--CGDLTGPSGVILSD----- 1218
DB 144 VRATTSRTERIW--PGVIVPVYIGNFTGTQRAIFKQAMHWEKHTCVTFERTDEE 199
QY 1219 -----NY-----PEPYRPGKED-----WKVYSPDVYA 1243
DB 200 SPVFSYRTGCCSYGRRGGPOAISIGNCKDFGIVAHELGVGFWEHETRPDDQH 259
QY 1244 LVFNIFNLEPG--YDFLHIYDGRDLSPLIGSFYGSQLPKRIBSSNSLFLAFPSDASVS 1301
DB 260 VTIIRRENIOPGOEYNFIAKMEAGVS--SLGERTY-----DPSIINHAYRNTS-- 304
QY 1302 NAGFVIDYTNPRESCDFPSIKNGTR--VGSDLKLGSSVTVYCHGGEVEGETSLCIL 1359
DB 305 -RGVFLD-TILPRRD-----DNGVPRPTIGQVRILSQGDIQAARKLYK----- 344
QY 1360 GPQKPYMNNPRVYCTAPCGGQYVSGDGVLSFNYPONTYSGOICLYFTVY--PKDYVY-- 1416
DB 345 -----CPA-CSETLQDTTGNFSAGFPNGYSYSHCWIRISVTPREKTIILN 389
QY 1417 FGGAFAPHTAL--NDVVEVHDGHSOHSRLSLSSGSHTEGSLPLATSNOLVLIKESAKGLA 1474
DB 390 FTSMDLFKSLCWDYVEIRIDGWRKAPLGRFCGDKIPESL--VSSDSRLMWEFRSSSSS 448
QY 1475 PARGFHEVYOAVPRTSATQCSSVPEPRYGRKLGSDSVGAIIVFECNSGYALOGSPERIC 1534
DB 449 LGKGFVAYEAM----- 460
QY 1535 LPVPGLAQNANVAPTCVVPCCGNLTERKGTIISPGPEPEYLSNLNCWKIVVPEAGIQ 1594
DB 461 -----CGGDITKDAQOISPNVPDDYRPSKECVMWRITVDPDGHVG 500
QY 1595 IOVVSFVTEON--WDSLEVPDQADNTVMTLGSFGTTPVPLALNSTNSDNLHYHFVSDIS 1650
DB 501 LTRQSFIEIRHSDCAIDYLSIRDPEDSTLIGHFCYERPEAVKSSANLWKFVSDGS 560
QY 1651 USAAGFLEKYKTVGLSSCPPEAVPSNGVKTGERVLYVDVVSF--QCEPGYALOGHAHISC 1708
DB 561 INKAGFAANF--FKVEVDCSWPDHG--GCEQRCVNTLGSYCAODPYELAA----- 608
QY 1709 MPTGTRRANTPPPLCTAOCGCTVEEMEGVLSGFGPNTYSNDCSKIALPYVGFQAHIQ 1768
DB 609 -----DKTCEVACGCFITKNGTITTSQWPEYETLNKNCQWQVAPVQYRISLQ 658
QY 1769 FLNFTSEPN--HDVIEINNGPYETSRMMGRSGSLPESLSTSHETTIVYFHSDSQSN 1824

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RESULT 14
US-09-285-385C-4
; Sequence 4, Application US/09285385C
; Patent No. 6579702
; GENERAL INFORMATION:
; APPLICANT: Greenspan, Daniel S.
; APPLICANT: Scott, Ian C.
; APPLICANT: Thomas, Christina L.
; TITLE OF INVENTION: MAMMALIAN TOLLOID-LIKE GENE AND PROTEIN
; FILE REFERENCE: 960296.96111
; CURRENT APPLICATION NUMBER: US/09/285,385C
; CURRENT FILING DATE: 1999-04-02

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Db 659 FEAFLENDVCKYDFVEVRSGLSPLDALKHGFCSERPEVITQSSNNMRVEFSDNTVS 718
QY 1825 RRGFLTEYQAYELQECPPDEPPANGIVAGAGYNGQVTFECLPGYOL--TGHEVLTCQH 1882
Db 719 KRGFALHFFS--DKDECARD---NGCCOECVNTFGSLCRGRNGYRLHENGH---DCK- 769
QY 1883 GTNRWMDHPLPKCEVPCGNGITSSNGITVSPGSPSPSSODCWMLTVPICGHVRLNLS 1942
Db 770 -----EAGCAYKISSAEGITLMSFNMWPKYPSRKECTWNISSTRGHRVKITFS 816
QY 1943 LLQTEP---SGDFTTWGPOQAPRLGVFTSRMAKTYVQSSNOVLKFKHDAATGCI 1998
Db 817 EFEEIOHOECAYDHELEVDGTDSLAPILGRFCGSKKDPVVAATSSILFRYSAS---V 873
QY 1999 FAIPSAVPLTKCPRPTILPAHAAVTEENEFNIGDIYARCLPPTVGNELTKCKICTY 2058
Db 874 ORKGFQAVHSTEC-----GGRLKA-EVQTKELYSH 902
QY 2059 LQFSGPPICEVHCPTNELLTDSYVILSGSPGSPYFQOTCSVLVREVPDYNISLTVEX 2118
Db 903 AQFG-----DNNYTSQARCDMWIVAEDGYVELIFRT 934
QY 2119 FLSEKO---YDEFEIPDPSGQSPPLKALSGNTSAPL-IVTSSNSVYLKRWSDHAAYNR 2173
Db 935 FEVEEADCGYDFMEAYDYDSDAPRLGRFCG--SGPLEEITYSAGDSLMIRFHTDITNK 992
QY 2174 KGFIRYSA 2182
Db 993 KGFHARTIS 1001

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RESULT 15

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US-08-991-408-2
; Sequence 2, Application US/08991408
; Patent No. 6008017
; GENERAL INFORMATION:
; APPLICANT: ARLETH, ANTHONY J.
; APPLICANT: WILLETTTE, ROBERT N.
; APPLICANT: ELISHOURBAGY, NABILI A.
; APPLICANT: LI, XIAOTONG
; TITLE OF INVENTION: HUMAN CARDIAC/BRAIN TOLLOID-LIKE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RAYNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/991,408
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/034,471
; FILING DATE: 02-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: ATG-50038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

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;
; LENGTH: 1013 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-991-408-2

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Query Match 4.5%; Score 769.5; DB 3; Length 1013;
Best Local Similarity 24.6%; Pred. No. 1.8e-50;
Matches 245; Conservative 131; Mismatches 331; Indels 287; Gaps 33;

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QY 879 NNHECIYSIOTOPGKGIQKARAFELSEGADVLYKVDGNNNSARLLGV-PSHEMMQVTIN 937
Db 258 DNHVTLIRENIQPGQ-----EYNFLMEPEGANNS--LGERYDFDSIMHYARN 302
QY 938 STSSSLMDLFDIDAENTSKGFEIHSSPELICKEDPG-TPKFGYKVH-DEGFAGSSVSF 995
Db 303 TFSRGWFLDTILPSR-----DNGIRPALGQRTRLSKDIAQA----- 340
QY 996 SCDPGYSLGSEBELCLSGERTWDRPLPTCYAECGGTYRGVSGCVLSFGYPAPYENHL 1055
Db 341 -----RKL YRCPA-CGETLQ--BSNGNLSPGFPNGYPSYT 373
QY 1056 NCIIWTIEABAGCTIGLHFLVPDTEEV---HDVLRIWDGPFVSGVYLKXELSPALPKDLH 1111
Db 374 HCIWRVSTPRGKIYVNTFTMLYKSSLCWYIYIEVRDGYWRKSPILGRFCGDKLPEVLT 433
QY 1112 STFNSVYLOFSTDFFTSKQGFALQPSVSTATSCNDPGIPQNGSRSGDSWEA-GDSTVFGC 1170
Db 434 STDSRMWIEF-----RSSNMVGKGAAYVE- 459
QY 1171 DPGVALQGSABEISCVKIENRPFQPSPTCLAPCGGDLTGPBGVLSPPYPPYPRGEC 1230
Db 460 -----AICGEIRKNEGQIQSPYPPDYPRMKEC 488
QY 1231 DWKVTVSPDYVALVNIENFNEP---GYDFLHIYDGRDSLPLIGSFYGSQLPRIESS 1286
Db 489 VKKITVSESYHGLFQFSGFEIERHNCAYDYLEVADGTSENSPLGRGCGYKPKPDIINST 548
QY 1287 SNLSPLARSDASVSNAGFVIDYTENPREBSCDPSISNGRIVSGDLKLGSSVTVY---C 1343
Db 549 SNTLWMKFEVSDGTAKGAFANFFKE-EDECKAP-----DRGCEGRCLNLTLSGYCAC 601
QY 1344 HGVYEVEGTSLSCILPGDGKPVNMNPRPVCTAPCGQGYVSGDVVLBPVNPONTTSQI 1403
Db 602 EPGYE-----LGRD-----RSCBAACGGILTKANGITTTGPKXEPYNNK 643
QY 1404 CLYEVTVPKDYVVFQGFAPFHTALNDV-----VEVHDGSHQHSRLLSLGSHTGESLPL 1458
Db 644 CWMQVVAFTQYRISVYKFEFFLEGNBVCYDVEIWSGLSSESKLHGKFCGALEVEYI-T 702
QY 1459 ATSNQVILKFAKGLAPARGF--HFVYQAVRTSTATQCSSYVPEPRYGRQLGSDSVGAIY 1516
Db 703 SQFNMRLEPKSDNTVSKKGFRAHF-----SDKDECS--KNGGQCHCVNMGSYM 753
QY 1517 RFECNSGYALQGS---PEIECLPVPGALAOMNVSAPCVPCGGNLTERRGTILSPGP 1572
Db 754 -CQCGNGFVLHNDKHDCKEAC-----EQKHSPS-----GLITSPWP 791
QY 1573 EPYLNSLNCVKKIYVBSAGIQLIOVSVFTBON---WDSLEVPDADNTVMTLGSFSGT 1628
Db 792 DKYPSRKECTWEISATPGHRIKLAFFESEFIEQHOECADVHLEVDGETEKSPILGRLCGN 851
QY 1629 TVPALINSTNOYLHFPSDISVSAAGHLEKYTVGLSSCCEPRAVPSNGVCTGERIYVND 1688
Db 852 KIPDELVAITGKMFRRFVSDASVQKGFQATHST----- 885
QY 1689 VVSFQCEPGVALQGHAIHSCMPTVRRWNYPPPLCIAOCGGTV--EEMEGYILSPFGP- 1745
Db 886 -----ECGGRLLAESKPRLLYHQAQGD 908
QY 1746 -NYSNMDCSWKILPVGFGAHIOFLNFSTEP---NHDYIEINNGPYETSRMMGRFSGS 1800

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Db	909	NNYGVDCMVLVSRGRLBJSFQTFEVEEADCGYDYVBLFDGLDSTAVGLGRFGS	968
Qy	1801	ELPSSLSTSHETTVFHSDDSONRPGFKLEYOA	1834
Db	969	GPPEIYISIGDSVLHFDHDDTINKKGFHIRYKS	1002

Search completed: October 18, 2004, 10:26:21
Job time : 74 secs

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Alignment Scores:

Pred. No.:	0	Length:	10136
Score:	16985.00	Matches:	3104
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-016-248-2 (1-3104) x AX685957 (1-10136)

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QY 1 MetAlaGlyAlaProProAlaLeuLeuProCySerLeuIleSerAspCys 20
DB 1 ATGGGGGGGGCCCCCCCCCGCTTGGCTGCTTCAGTTTATTCAGTCTGCT 60
QY 21 AlaSerAspGlnArgHisSerValGlyValGlyProSerGluLeuValLeuGlnIle 40
DB 61 GCTACCAATCCAGCCGACTCCGTGGCGCTAGGACCTCCGAGCTACAGAACCAATT 120
QY 41 GluLeuIleSerAspGlyValIleLeuMetProSerIleAspAspSerGlnIleThrSer 60
DB 121 GAGTTGAAGTCTCCAGAGTGTAGTGAAGTGTATCCCAAGAACAAACAGCCAGAGAGCTCT 180
QY 61 ValLeuThrGlnValGlyValSerGlnGlyHisAspMetCysProAspProGlyIlePro 80
DB 181 GTGTTAACTCAGGTGGTGTGTCCCAAGACATATATGTGTCCAGACCCCTGGCATACCC 240
QY 81 GluArgGlyLeuArgLeuGlySerAspPheArgLeuGlySerSerValGlnPheThrCys 100
DB 241 GAAAGGGGCAAAACATAGGCTTCGAAATTTCCAGTTAGATTCAGCGTCCAGTTCTACCTGC 300
QY 101 AsnGlnGlyIleAspLeuGlnGlySerIleAspGlyIleThrCysMetLeuValSerAspMet 120
DB 301 AACACGGGCTATGACTCTCAAGAGGCTCCAAAGGAGATCACTGTATGAAAGAGACGACATG 360
QY 121 PheAlaIleThrSerAspHisArgProValCysArgAlaArgMetCysAspAlaHisLeu 140
DB 361 TTTCGGGCTGAGAGCCAGACAGGCGCAGTCCGAGCCCGCATGTGTGTGCCCACTT 420
QY 141 ArgGlyProSerGlyIleIleThrSerProAspPheProIleGlnIleAspAspAspAla 160
DB 421 CGAGGCCCTCGGCGCATCATCACTCCCAATTTCCCACTTCAAGTATGACAAACATATGCA 480
QY 161 HisGlyValIleThrIleIleThrAlaLeuAspProSerIleValIleLeuAlaPheGln 180
DB 481 CACTGTGTGATGATCAATCAGACACTCAACCCCTCCAAAGGTGATCAAGCTCGCTTTGAG 540
QY 181 GluPheAspLeuGluArgGlyIleAspThrLeuThrValGlyAspGlyGlnAspGly 200
DB 541 GAGTTTGAATTTGAGAGGGGCTATGACACCTTACCGGTGATGTGTGTGATGAGATGGG 600
QY 201 AspGlnIleThrValLeuIleThrMetSerGlnAspAlaCysSerAspSerProHisThrPro 220
DB 601 GACCAGAAAGACAGTCTCTCATGTCTCAAAATGCTCGAGATGACAGCCCTCACACCCCA 660
QY 221 GlySerArgIleProGluSerMetSerGlyAspIleIleThrArgGlnIleThrValLeu 240
DB 661 GGGTCTCGCATCCAGAGACATGCTGTGGGACATGTGAGGAGAAAGAGACTGACTT 720
QY 241 GluIleCysArgAspIleSerSerSerAspAlaArgSerGlySerValArgIleSerPro 260
DB 721 GAGATCTGTGTGATCAATTTGACATTCAGATTCAGATTCAGATTCAGATTCAGATTC 780
QY 261 LeuThrSerAspAlaValGluLeuValAlaProGlyIleThrGluIleGlnGlnIleSerCys 280
DB 781 AAACATTTCAATCTGTGAACTTTGTTGCTCTCGGAGACAGAGATGAGAGGAGGAGCTTGC 840
QY 281 GlyAspProGlyIleProAlaIleArgArgGlnGlySerArgPheHisIleGlyAsp 300
DB 841 GGTGACCTCGCATCTGCTGATGTGCGCGAGAGAGGCTCCCGGTTTCCACCACTGATAC 900
QY 301 ThrLeuIlePheGlnIleCysGlnProAlaPheGlnLeuValGlyGlnAlaIleThrCys 320

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DB 901 ACACTCAAGTTTGAAGTCCAGCCCGCTTTGAGCTGTGGAGACAGAAAGCAATCATATGC 960
QY 321 GlnIleAspAsnGlnIleThrSerAlaIleCysProGlyCysValPheSerCysPheAsn 340
DB 961 CAABAAGATTAACCAATGCTGCGCTTAAGAGCCAGAGGTGTGTCTTCCGTCTTCAAC 1020
QY 341 PheThrSerProSerGlyValIleLeuSerProAsnIleProGluAspIleGlyAsnHis 360
DB 1021 TTCACCGCCCGCTGTGGGTGTCTGTCTTCCCACTACCAAGAGACTATGGCAACAC 1080
QY 361 LeuHisCysValIleLeuIleLeuAlaArgProGluSerArgIleHisLeuAlaPheAsn 380
DB 1081 CTCACATGTGTCTGTGCTATCTTGCACAGGCTTGAGAGCCGATCCACTGTGCTTCAAC 1140
QY 381 AspIleAspValGluProGlnPheAspPheLeuValIleIleAspGlyValAlaThrAlaGln 400
DB 1141 GACATTGAGTGGAGGCTCAAGTTATTTCTGTGATCAACAGATGGGAGCCAGCCAG 1200
QY 401 AlaProValLeuGlyIleThrPheSerGlyValGlnIleLeuProSerSerIleThrSerSerGly 420
DB 1201 GGGCCGCTCTGGGACCTTCTCAGAGAAACAGCTTCCCTCCATCATCAAGCAGTGC 1260
QY 421 HisValAlaArgLeuGluPheGlnIleThrAspHisSerThrGlyValArgGlyPheAsnIle 440
DB 1261 CAGTGTGGCCGCTCTGATTCAGATTCAGACTCACTTCAAGGAGAGAGGAGGCTTCAACATC 1320
QY 441 ThrPheThrThrPheArgHisAsnGluCysArgProAspProGlyIleProValAsnGlyHis 460
DB 1321 ACTTTTACACCTTCCAGACACAGAGGCGGAGCTTGGCGTTCCAGTAAATGGGCAAA 1380
QY 461 ArgPheGlyAspSerLeuGlnIleGlySerSerIleSerPheLeuCysAspGlnGlyPhe 480
DB 1381 CGGTTTGGGAGAGCTTCACTGAGGAGCTTCACTTCTTCTTCTGTGAGAAAGGCTTC 1440
QY 481 LeuGlyIleThrGlnIleSerGluThrIleThrCysValIleLeuGlySerValIleValIle 500
DB 1441 CTTGGGACTCAGGGGCTCAGACATCATCACTCGGCTTCAAGAGAGGAGGAGGCTGTG 1500
QY 501 AsnSerAlaValIleLeuArgCysGlnAlaProCysGlyGlyHisLeuThrSerProSerGly 520
DB 1501 AACAGCGCTGTGCGGTGTGAGAGCTCCGTGTGTGTCTCACTGAGCTTGGCCAGCGGC 1560
QY 521 ThrIleLeuSerProGlyIleThrProGlyIlePheThrIleAspAlaLeuSerCysAlaIleVal 540
DB 1561 ACGATTCCTCTCTCGGGCTGCGCTGCTTCAAGAGATGCTTGAAGCTGTGAGG 1620
QY 541 IleGluAlaGlnProGlyIleProIleIleIleThrPheAspArgPheIleThrGluVal 560
DB 1621 ATTGAGGCCAGCCAGGCTACCCCATCAAAATCACTTGCAGATTCAAAACCGAGGCTC 1680
QY 561 AsnIleAspThrIleGluValArgAspGlyArgThrIleSerAlaProLeuIleGlyVal 580
DB 1681 AACATGACCTCTGAGAGATGAGGATGGGAGCTTAACAGAGCCCTTGAATGGGGGTT 1740
QY 581 TyrHisGlyIleThrGlnValProGlnPheLeuIleSerThrSerAsnIleThrLeuIleLeu 600
DB 1741 TACCAGGAGACCCAGGTTTCCCAAGTCTCATAGAGACAGCAACTCACTTCACTCTC 1800
QY 601 PheSerThrAspIleSerHisSerAspIleGlyPheGlnIleLeuArgIleThrIleThr 620
DB 1801 TTCTTACCAAGAGTCACTCGGACATCGGCTTCCAGCTCCGCTATGAGACTATTAACA 1860
QY 621 LeuGlnSerAspHisCysLeuAspProGlyIleProValAsnGlyGlnArgHisIleGlyAsn 640
DB 1861 CTGCAAGTCAACACATCTGTGTGATTCAGAGATTCAGTAAATGAGACAGGCTCATGGGAAT 1920
QY 641 AspPheThrValGlyAlaLeuValIleThrPheSerCysAspSerGlyIleThrLeuSerAsp 660
DB 1921 GACTTCTACAGTGGCGCGGTGTGACCTTCAAGTGTGACTCGGGCTTACACATTAATGAG 1980
QY 661 GlyIleProLeuGlnIleCysGlnProAspPheGlnIleThrSerArgAlaLeuProSerCysGlu 680
DB 1981 GGGGAGCTCTGAGAGTGTGAGCCAACTTCAAGTGAAGCGGCGCTTGCACAGTGTGAA 2040

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QY	681	llaleucysgilygilypheiilegnglysersegiythrilleuaseerproglyphea	700
Db	2041	gctctctgtggggctgtattccaaagcctccagctggacatctgtgtccagggttccct	2100
QY	701	AspPheTyProAsnAsnLeuAsnCybThrTrpIlellegluthrSerHisgLYLysgLY	720
Db	2101	GACttTtTACCCCAACtTGAACtTGACctTGAAATTATCGAAACtTCCATGGCAAGGT	2160
QY	721	ValPhePheThrPheHisThrPheHileuGLusergiyHisaapTYrLeuLeuIleThr	740
Db	2161	GTGtTCTTCACtTTCACACcCTTCACcCTGGAAAGTGGCCATGACTACtTCTCATACT	2220
QY	741	GLuAnsgLYserPheThrGLnProleuArgGLnLeuThrGLySerArgLeuProAlAPro	760
Db	2221	GAGAAcGGCAcCTTCACCCACcCCCTGAGGACGTACTGGAATCTGGCTGCAGCTCC	2280
QY	761	IlleSerAlaGLyLeuTYrGLyAsnPheThrAlaGLnValArgPheIlleSerAspPheSer	780
Db	2281	ATCAGCGCTGGGGCTGTATGGCAACTTCACtCCcCGAGGCTCCCTTCATCTGATTTCTCC	2340
QY	781	MetSerTYrGLyPheAsnIleleThrPheSerGLyTrAspLeuGLnProCyGLnGLu	800
Db	2341	ATGTCATATGAAAGGATTCACATCACTTCCTCAAGTACGACTTGAGACCCCTGTGAGAG	2400
QY	801	ProGLnValProAlaTYrSerIlleArgLYsgLYeuGLnPhaGLyValGLyAspThrLeu	820
Db	2401	CCCGAGGTCCCAcGCTTACAGCATCCGGAAGGGCTTGCAgTTTGGTGTGGCGACACCTTG	2460
QY	821	ThrPheSerCyPhePheProGLyTYrArgLeuGLyThrAlaArgIlleThrCyLeuGLy	840
Db	2461	ACCTTCTCTCTCTCTCCCGGGATCCGTGTGAAGGGCACCGCCCGATCACCTGCTGGGG	2520
QY	841	GLyArgArgArgLeuTrpSerSerProleuProArgCybValAlaGLnCYsGLyAsnSer	860
Db	2521	GGCAGACGGCCCTGTGGAGCTCGCCTTGCcAAGTGTGTCTGAGTGTGGGAATTCA	2580
QY	861	ValThrGLyThrGLnGLyThrLeuLeuSerProAsnPheProValAsnTYrAsnAsn	880
Db	2581	GTCACAGGCACTCAAGGATCACTTGTCTGCCCAACTTCCGTGMACTAACATACAT	2640
QY	881	HisGLnCYsIlleTYrSerIlleGLnThrGLnProGLyLYsgLYIleGLnLeuLYAlaArg	900
Db	2641	CATGATCACTTACTTCATCCATCCAGACCCAGCGAGGAAGGAATTCAGCTAAAGCCAGG	2700
QY	901	AlaPheGLnLeuSerGLnGLyAspValLeuLYsValTYrAspGLyAsnAsnAsnSerAla	920
Db	2701	GCATTCGAACCTCTCCGAAGAGATGTCTCAAGGTTTATGATGGCAACAACACTCGGC	2760
QY	921	ArgLeuLeuGLyValPheSerHisSerGLuWecheeGLyValThrLeuAsnSerThrSer	940
Db	2761	CGTTTGCAGGAGGTTTATGACATTCCTAGATGAGGGGGAGACTTTGAAACAGACAATCC	2820
QY	941	SerSerLeuTrpLeuAspPheIleThrAspAlaGLuAsnThrSerLYsGLyPheGLnLeu	960
Db	2821	AGCACTCTGTGGCTTGAATTCTCATCTAGTGTGAHAACACACGACAGAGGCTTTGAACGTG	2880
QY	961	HisPheSerSerPheGLnLeuIleLYsCYsGLuAspProGLyThrProLYsPheGLyTYr	980
Db	2881	CACtTTCACAGCTTGAACtTCACTCAAAATGTAGAGACCAGGAACCCCAAGCTTTGGCTAC	2940
QY	981	LYsValHisAspGLnGLyHisPheAlaGLySerSerValSerPheSerCyAspProGLy	1000
Db	2941	AAGGTTCATGATGAAGGTCAATTTCACAGAGACCTCGTGTCTTCAGCTGTGACCTCGGA	3000
QY	1001	TYrSerLeuArgGLySerGLnLeuLeuLeuCYsLeuSerGLyGLuArgArgTYrTrpAsp	1020
Db	3001	TACACCTCGCGGGAGTATGAGAGAGCTCGTGTGTCTGATGTGAGAGCGCGGACCTGGGAC	3060
QY	1021	ArgProLeuProThrCybValAlaGLnCYsGLyGLyThrValArgGLyGLuValSerGLy	1040
Db	3061	CGGCTCTTGCACCTGTGTGTGGCCAGATGTGGAGGACATGTAGAGAGAGAGTGTGGGG	3120

QY	1041	GlntAlleuSerProGlyYrProAlaProThyGlnHisAsnLeuAsnCySileTrpThr	1060
Db	3121	CAGGtGCTGCACCCGGGATCCAGGCTCCATGAACAACATCTCAACTGATGTGACC	3180
QY	1061	IlleglunAgluaIagIyCyThrlEglYLeuHisPheLeuValPheAsPThrGluGlu	1080
Db	3181	ATCGAAGCAGAGGCCGGCTGCACCATTTGGCTACACTTCTGGTGTTCACACAGAGAG	3240
QY	1081	ValHisapValLeuAargIleTrpAspGlyProValGluSerGlyValLeuLeuYegLu	1100
Db	3241	GTTCAACGACGtGCTGCATCTGGGATGAGGCGCTGTGAGAGAGCGGGCTTCGCTGAAGAG	3300
QY	1101	LeuSerGlyProAlaLeuProValAspLeuHisSerThrPheAsnSerValValLeuGln	1120
Db	3301	CTGAGTGCCCGGGCCCTGGCCCAAGACCTGTATGACCTTCAACTGAGTGCTCTGACAG	3360
QY	1121	PheSerThrAspPhePheThrSerYegGlnYpHeAlaIleGlnPheSerValSerThr	1140
Db	3361	TTTCAGCACTGACTTCTTCACCGACAGAGGGCTTTGGCATTCATTTCAGTGTCCACA	3420
QY	1141	AlaThrSerCyAsaAspProGlyIleProGlnAsnGlySerAargSerGlyAspSerTrp	1160
Db	3421	GCAAGCTCTGCATATGACCTGGGATCCCGAGAAATGGAGTCCGAGTGGTGAACAGTTGG	3480
QY	1161	GluAlaaglYAspSerThrValPheGlnCyAspProGlyTrValaLeuGlnGlySerAla	1180
Db	3481	GAAGCGGGCGACTCCACAGTGTTCCAGTGATACCCTGTCAACGGCTGCAGGGAGATGCA	3540
QY	1181	GluIleSerCyValuValYleGlnAsnAspPhePheTrpGlnProSerProProThrCys	1200
Db	3541	GAGATCAGCTGTGTGAAGATGAACAAGGTTCTTCTGGCAGGCCAGCCGCGCAACATGC	3600
QY	1201	IleAlaProCySglYgIyAspLeuThrGlyProSerGlyValIleLeuSerProAsnTrp	1220
Db	3601	ATCGCTCCCTGGGGGAGACCTCAACAGAACATCTGGAATCATCTGCATCCCAATATAC	3660
QY	1221	ProGluProGlyrProProGlyYegGluCyAspTrpIlyValThrValSerProAspTrp	1240
Db	3661	CCAGAACCTTACCCCGCAGGACGAAGTGTGACTCGAAAGTACCGTCTCCACGACTAC	3720
QY	1241	ValIleAlaLeuValPheAsnIlePheAsnLeuGluProGlyTrAspPheLeuHisIle	1260
Db	3721	GTCACTGCCCTGGATTTTAACTATTAACTTGAAGCTTGCACTTGAATCTTCTCATATC	3780
QY	1261	TrAspGlyAArgAspSerLeuSerProLeuIleGlySerPheTrYGlySerGlnLeuPro	1280
Db	3781	TACACGAGCGGAGACTCTCTACGCCCTCTATAGAAAGCTTATGGCTCCCACTCCA	3840
QY	1281	GlyAArgIleGluSerSerSerAsnSerLeuPheLeuAlaPheArgSerAspAlaSerVal	1300
Db	3841	GGCGGCATTTGAACACAGACGACACAGCTCTTCCCTCCGACACGATGCATCTGTG	3900
QY	1301	SerAsnAlaGlyPheValIleAspTrpThrGlnAsnProAArgGluSerCySAspAspPro	1320
Db	3901	AGCAATGCTGGCTTCGTATTGACTATACAAACCCGCGGAGTATGTTGATCTT	3960
QY	1321	GlySerIleLeuAsnGlyThrArgValGlySerAspLeuYleGluGlySerSerValThr	1340
Db	3961	GGTTCATCAAGAACGCGACACGGGTGGGTCCCACTCGAAGCTGGGCTCTCCGTACCC	4020
QY	1341	TyrTrpCySHisGlyGlyTrpGluValGlnGlyThrSerThrLeuSerCySileGluGly	1360
Db	4021	TACTACTGCCACGGGGGCTACGAGATGTAGGGACCTCGAACCTCGACTGATCTGTGGG	4080
QY	1361	ProAspGlyYleProValITrPAsnAsnProAArgProValCySThrAlaProCyGlyGly	1380
Db	4081	CCTGATGGGAAGCCCGTGTGGAACAATCCCGGCGCAATCTGCACAGCCCTCTGTGGGAGA	4140
QY	1381	GlnTrpValGlySerAspGlyValValLeuSerProAsnTrpProGlnAsnTrpThrSer	1400
Db	4141	CAGATGTGGGTTTGGACGAGAGTGTCTTGTCTCCCACTACACCCCGAAGTACACCACT	4200
QY	1401	GlyGlnIleCySLeuTrpPheValThrValProIlyAspTrpValValPheGlyGlnPhe	1420

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Db 4201 GGCAGATCGCTGTAATTTGTAATCTGTGCGCCAGAGCATATGATGATGTTGGCCAGTTC 4260
Qy 1421 AAlpPhePheHisThrAlaLeuAenAapValValGluValHisAaspGlyHisSerSerGlnHis 1440
Db 4261 GCGCTTTTTCACACGCGCCCTCAACGACGATGAGAGTTTCAACGACGCGCACAGGCCAGCAC 4320
Qy 1441 SerArgLeuLeuSerSerLeuSerGlySerHisSThrGlyGluSerLeuProLeuAlaThr 1460
Db 4321 TCGCGGCTCTCAAGCTCCCTCTCGGGCTCCCATACAGAGAGATCACTGCTTGGCCACC 4380
Qy 1461 SerAenGlnValLeuLileysPheSerAlaLysGlyLeuAlaProAlaArgGlyPheHis 1480
Db 4381 TCCATACAGATCTCATTAAGTTACGCGCAAGCCCTCGACACCGACGAGCTTCCAC 4440
Qy 1481 PheValTyrGlnAlaValProArgThrSerAlaThrGlnCysSerSerValProGluPro 1500
Db 4441 TTTGCTACCAAGCGATCTCTGAAACAGCGCACGACGACGACGACGCTGCTGCGGAAACC 4500
Qy 1501 ArgTyrGlyLysArgLeuGlySerAaspPheSerValGlyValAlaIleValArgPheGluCys 1520
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Qy 1521 AenSerGlyTyrAlaLeuGlnGlySerProGluLileGlnCysLeuProValProGlyVala 1540
Db 4561 AACTCGGCTATGCGCTCGAGGGGTGCGCACAGATCGAGTGCCTCCCTGCGCTGGGGCC 4620
Qy 1541 LeuAlaGlnTyrPheAenValSerAlaProThrCysValValaProCysGlyValAenLeuThr 1560
Db 4621 TTGGCGCCATGGAATGTTCTACGCGCCACGATGATGCGGTGGAGGCAACCTTCACA 4680
Qy 1561 GluArgArgGlyThrIleLeuSerProGlyPheProGluProGlyLeuAenSerLeuAen 1580
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Qy 1581 CysValTyrPheLysIleValValProGluGlyValaGlyIleGlnIleGlnValValSerPhe 1600
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Qy 1641 LeuTyrLeuHisPheTyrSerAaspIleSerValSerAlaAlaGlyPheHisIleuGlnIlyr 1660
Db 4921 CTCTACTTCTATTTCTACTCAATATACGCTATCTGCAAGCTGCTTCCACTTGAAGTAC 4980
Qy 1661 LysThrValGlyLeuSerSerCysProGluProAlaValaProSerAenGlyValIlyThr 1680
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Qy 1681 GlyValArgTyrLeuValAenAaspValaValSerPheGlnCysGluProGlyTyrAlaLeu 1700
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Db 5101 CAGGGCCACGCGCACATCTCTGCAAGCCCGGAAACAGTCCGCGATGAACTACCTCTCT 5160
Qy 1721 ProLeuCysIleAlaGlnCysGlyGlyThrValaGluGluMetGluGlyValIleLeuSer 1740
Db 5161 CCACTCTGATTTGCAAGTGTGGGGAACAGTGAAGATGAAGAGGGGTGATCTCTGAGC 5220
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Db 5401 GAGCTTCCAAAGCTCCCTCTCTCAAGTCCAGAGACCAACCGTGTATTTCCACAGGAC 5460
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Db 5461 CACTCCCAAAATCGGCAAGATTCAGAGTGAAGTATCAGGCTTATGAATTCACAAAGTGC 5520
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Db 5521 CCAGACCCAGAGCCCTTTTCCAAATGCAATGCAATGGAAGGAGCTGGCTACAAAGTGGACAA 5580
Qy 1861 SerValThrPheGluCysLeuProGlyTyrGlnLeuThrGlyHisAProValLeuThrCys 1880
Db 5581 TCAGTACCTTGAAGTGCCTCCCGGGTATCATTAATGACTGGCACTGCTCCTCACGCT 5640
Qy 1881 GlnHisGlyThrAenArgAenThrAaspHisAProLeuProLysCysGluValaProCysGly 1900
Db 5641 CAACATGGCAACCAACCGAAGCTGGAGCAACCCCTGCGCAAGTGAAGTCCCTTGTGGC 5700
Qy 1901 GlyAenIleThrSerSerAenGlyThrValaTyrSerProGlyPheProSerProTyrSer 1920
Db 5701 GGGAACTACACTTCTTCCAAAGGACGTGTATCTCCCGGGGTCTCCCTAAGCCGTACTCC 5760
Qy 1921 SerSerGlnAenProCysValaTyrLeuLileThrValaProIleGlyHisGlyValaArgLeuAen 1940
Db 5761 AGCTCCAGAGATGATGCTGCTGATCACTCCCTGCGCAATGGCGCTGCTCCCTCAAC 5820
Qy 1941 LeuSerLeuLeuGlnThrGluProSerGlyAaspPheIleThrIleTyrAaspGlyProGln 1960
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Qy 1961 GlnThrAlaProArgLeuGlyValaPheThrArgSerMetAlaLysLysThrValaGlnSer 1980
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Qy 1981 SerSerAenGlnValaLeuLeuLysPheHisAArgAapAlaAlaThrGlyGlyIlePheAla 2000
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Qy 2061 PheGluGlyProProProIleCysGluValaHisCysProThrAenGluLeuLeuThrAap 2080
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Qy 2081 SerThrGlyValaIleLeuSerGlnSerTyrProGlySerTyrProGlnPheGlnThrCys 2100
Db 6241 TCCACAGGCGTATCTCTGAGCCAGAGACTACCTCGAAGATTAATCCCAAGTTCCAGACCTGC 6300
Qy 2101 SerTyrLeuValaArgValaGluProAaspTyrAenIleSerLeuThrValaGluTyrPheLeu 2120
Db 6301 TCTTGGCTGATGAGATGAGAGCCGACATTAATCATCTCTCCATCAAGTGAAGTACTTCTTC 6360
Qy 2121 SerGluLysGlnTyrAaspGluPheGluIlePheAapGlyProSerGlyGlnSerProLeu 2140
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QY 2161 ValTyrLeuArgTyrPheSerSerAspHisAlaTyrAsnArgIleGlyPheValIleArgTyr 2180
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QY 2581 AsnHisGlyPheTyrLeuLeuGlyIleThrProValLeuSerCysGlnIleAspGlyIleThr 2600
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QY 2861 ValValIleIleSerAspPheMetTrrPheIleSerSerValThrTyrAlaCysLeuGlyIle 2880
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Db	9061	CCTACCTGTGCCCCCACTGACGAGGACGACGACGACGACGACGACGACGACGACGACGACG	9120	ATVSAATLTLRLISDYAVASQGHATAYELPSHTCGNPGRLNGIOGSPFNIGDK
Qy	3041	AlaLeuAspLeuProSerMetGlyTyrThrLeuIleThrProAlaArgAlaGlyAspPro	3060	VRSNCNLGFLRIGHAVLTCHGSNSATMDPFLSCRADADACGTLRQSGITLSPHF
Db	9121	GCCCTGTGTTTCCCTTCATAGGCTCAACAGCTCATTACTCTCTCTCTCTCTCTCTCTCTCT	9180	BEYHNNDCTTTLAELGDTLALVITFIOBDDGDFLEVTGTESSLMFTGASLPAP
Qy	3061	SerArgValAlaProSerThrAlaProAlaArgArgMetAlaAlaGlyAlaAsnArg	3080	VYSQNMCLHFTSDGNHRQGFSAQYOVKKQIELKSGVKKLMPKDKMSOKTSVLTQV
Db	9181	TCAAGGGTGGCTCGAGACACCGACCTGCAAGGGGATGCACTGCAAGGCAAGCCGC	9240	GVSGQNMCCPDGELPERGRUGSDRLSPSVQFTCNBEGYDLOGSKRTICMKVDMFAA
Qy	3081	ProSerAlaThrPheArgSerGlyProValGlyAspProSerThrLeuProGlySerHisArg	3100	MSDRPVCARAKCDHLRGPGLITSPNPIQYDNNAICWMLITLANSKYLKAFEE
Db	9241	CCATCTCTCTGAGAGTCCGGCCCACTGAGGACCCATCACTGACCCCGGAGCCACCCG	9300	FDLERGDTLTVGDDGDDOKTVLYLTGTSVPLDLYSTHOMMLFOTQSGSLKAFEE
Qy	3101	SerProLeuAspPro 3104		FASAYEIEQSGSCDPGIPAYGRREGSGFHGDTLKPCQAPFELVCGKATTCQKMG
Db	9301	TCAACCAAGCT 9312		MSAKKRGVSCFFNFTSPSGVYLSPNYPRDYGNHLHCWMLILAPESRHLAEFNDID
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LOCUS				MNSAVLRCEAPCGHILSPSGTILSPGMEFYKDALSCAWYLEAPGPKITFDRFK
DEFINITION				TEVNDTLEVDGRTYSAPLIGVHTGTPQPELITSTNYLILFSTGSHSDIGLOFL
ACCESSION				YETITLQSDHCLDPGIPVNGRGHNDPEVVALVPSQSGYTLSDGPELBEHPNOMS
VERSION				RALPSCFALCGGFTQSGSTLISGFPDPYPMNINCTMTITSHKGVFTFTHLE
KEYWORDS				SGHLYLITNGSFTQPLRQUTGSRILPAPISAGLYGNFTAOVRITSDMSYEGENIT
SOURCE				PSYDLEPCBEEVPAYSIRKQLOPFGVDTLTFSCFPYRLGELARITLCGRRLMS
ORGANISM				SPLPRCAECNSVVTGQTLSPNPNVNNHETYSIQTOGKQQLKARAEIS
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Db	3861	GAGGTGTGGGGCAGGAGTGGTCGTACCCGGGGTATCCAGCTCCCTATGAAACAATCTCCAC	392
Qy	1057	CysIleTyrThrIleGluIaIaGluIaGlyCysThrIleGlyLeuHisPheLeuValPhe	107
Db	3921	TGCATCTGGACCATCGAAGCAGAGGCGCGCTGCACTTGGGCTTACACTTCTCGTGTCTT	398
Qy	1077	AspThrGluGluValHisAspValLeuAlaGlyIleTyrAspGlyProValGluSerGlyVal	109
Db	3981	GAAACAGAGAGAGTTTACACAGCGTCCGCACTCTGGGAATGGCGCTGTGGAGAGAGCGGGATT	404
Qy	1097	LeuLeuLysGluLeuSerGlyProAlaLeuProLysAspLeuHisSerThrPheAsnSer	111
Db	4041	CTGCTGAAGAGACTGAGTGGCCCGCGCCCTGCCCAAGACTGATAGCACTTCAACTGC	410
Qy	1117	ValValLeuGluPheSerThrAspPheThrSerLysGlyIlePheAlaIleGlnPhe	113
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Qy	1137	SerValSerThrAlaThrSerCysAsnAspProGlyIleProGluAsnGlySerArgSer	115
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Qy	1177	GlnGlySerAlaGlnIleSerCysValLysIleGluAsnArgPhePheTyrGlnProSer	119
Db	4281	CAGGAAATGCGAGAAATACGCTGTGTGAAGATCGAACAAGATTCTTCTGGCAGGCCAAC	434
Qy	1197	ProProThrCysIleAlaProCysGlyGlyAspLeuThrGlyProSerGlyValIleLeu	121
Db	4341	CGGCAATGATGATGCTCTCCCTGGGGGAGACCTGACAGACCATCTGGATCATCTTC	440
Qy	1217	SerProAsnTyrProGluProTyrProProGlyLysGluCysAspTyrValThrVal	123
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Qy	1257	PheLeuHisIleIleTyrAspGlyArgAspSerLeuSerProLeuIleGlySerPheTyrGly	127
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Qy	1277	SerGlnLeuProGlyArgIleGlySerSerSerAsnSerLeuPheLeuValPheArgSer	129
Db	4581	TCCACAGCTCCAGGCGGATTTGAAAGCAGCAACAGCCCTTCTCTGCTTCGCAAGC	464
Qy	1297	AspAlaSerValSerAsnAlaGlyPheValIleAspTyrThrGluAsnProArgGluSer	131
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Qy	1317	CysPheAspProGlySerIleValAsnGlyThrArgValaGlySerAspLeuLysGly	133
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Qy	1337	SerSerValThrTyrTyrCysHisGlyTyrGluValaGlyIleTyrSerThrLeuSer	135
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS 1
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Carmen, S.J., Colman, S.D., Edinger, S.R., Ellemann, K., Gerlach, V.,
Gorman, L., Grosse, W.M., Guo, X., Hertrich, J.L., Kexuda, R.,
Lepley, D.M., Li, L., Macdougall, J.R., Millet, I., Pena, C.E.,
Peyman, J.A., Rastelli, L., Rieger, D.K., Shmukets, R.A., Smithson, G.,
Spreken, K.A., Stone, D.J., Tchernov, V.T., Vernet, C.A., Voss, E.Z.,
Zerhous, B.D., Zhong, H., and Zhong, M.
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Curagen Corporation (US)
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Q	y	1821	HIsSerGluAsnArgProglYpHeIleGluGluTYrGlnAlaTYrGluLeuGlnGluCys	1840
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 REFERENCE
 AUTHORS Sun, P.C., Uppaluri, R., Schmidt, A.P., Pashia, M.E., Quant, E.C.,
 TITLE Sunwoo, J.B., Gollin, S.M. and Scholnick, S.B.,
 Transcription map of the 8p23 putative tumor suppressor region
 JOURNAL Genomics 75 (1-3), 17-25 (2001)
 MEDLINE 21365705
 PUBMED 11472063
 REFERENCE 2 (bases 1 to 11580)

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 TITLE Sunwoo, J.B., Gollin, S.M. and Scholnick, S.B.
 JOURNAL Direct Submission
 Submitted (04-JAN-2001) Oncology, Washington University
 School of Medicine, Box 8115, 517 S. Euclid Ave, Saint Louis, MO
 63110, USA
 REFERENCE 3 (bases 1 to 11580)
 AUTHORS Tong, B. and Scholnick, S.B.
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 JOURNAL Submitted (28-JAN-2003) Oncology, Washington University
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Qy	2598	GlyThrThrPheArgPheArgPheArgProGlnCysLeuLeuValSerCysGlyHisProGlySer	2617
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Qy	2618	ProProHisSerGlnMetSerGlyAspSerTyrThrAlaGlyValAlaValAlaGlyTrpSer	2637
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Db	9169	ACCCACAGACATGGGTCTCCGCTTGAGTACATTAAACAAAGAGTCTTCCGCTTC	9228
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ACCESSION AY017475
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ORGANISM  Mus musculus
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AUTHORS  Sun, P.C., Uppaluri, R., Schmidt, A.P., Pashia, M.E., Quant, E.C.,
          1 (bases 1 to 11221)
          Sun, P.C., Uppaluri, R., Schmidt, A.P., Pashia, M.E., Quant, E.C.,
          2 (bases 1 to 11221)
          Transcription map of the 8p23 putative tumor suppressor region
          Genomics 75 (1-3), 17-25 (2001)
TITLE    JOURNAL MEDLINE 21365705
PUBMED   11472063
AUTHORS  Sun, P.C., Uppaluri, R., Schmidt, A.P., Davis, M.E., Quant, E.C.,
          Sunwoo, J.B., Gollin, S.M. and Scholnick, S.B.
          Direct Submission
          Submitted (09-JUN-2001) Otolaryngology, Washington University
          School of Medicine, Box 8115, 517 S. Euclid Ave, Saint Louis, MO
          63110, USA
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AX374891
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REFERENCE 1
AUTHORS Welcher A.A. and Elliott G.S.
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Amgen Inc. (US)
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ALLISGPAFLYLGHTRTPKYQVNGVAGHENSNGQASPENMVTNLIKPTBAKAVRFDI
TLNVTCTIV"

ORIGIN

Alignment Scores:

Pred. No.: 0
Score: 10737.00
Percent Similarity: 78.37%
Best Local Similarity: 63.60%
Query Match: 63.21%
DB: 6
Length: 10673
Matches: 1864
Conservative: 433
Mismatches: 567
Indels: 67
Gaps: 7

US-10-016-248-2 (1-3104) X AX374891 (1-10673)

QY	511	Cys61Ys61Yh1sleuthSerProSerGlyThh1leuSerProGlyTTPProGlyPhe	530
Db	1120	TGtGTGCACTGTGACAGCGCTCCAGGGAGTCATTTTGTCTCTGGATGGCAGGATAT	117
QY	531	TyrlsAhpAlaleuSerCyvalaTPVal11leG1uAlaGlnProGlyTTPPro1eLys	550
Db	1180	TATAGAGATTCTTACCTGTGTGAATGGATATATGAAAGCAAAACAGGCCACTATCAAA	123
QY	551	IlleThPheAspArgPheLysThrG1uValAsnTyrAspThrLeuG1uValArgAspGly	570
Db	1240	ATAACCTTTGACAGATTTACAGACAGAGGTCAATATTAAGAACCTTGAAGGTCAAGATGGG	129
QY	571	ArgThrTyrSerAlaProLeu1leG1yAlaTyrN1sG1YthG1nValProGlnPheLeu	590
Db	1300	CCAGCCAGGTTGCTGCTCCACGTGATCGGCGAGTACAGGACCCAGGCCACCCAGTTCTTC	135
QY	591	IlleSerThrSerAsnTyrLeuTyrLeuLeuPheSerThrAspLysSerH1sSerA1le	610
Db	1360	ATAGACACGGGAACTTCATATGACCTGCAATTCACACATGAAACAACAGCCGCTCCAGATCC	141
QY	611	GlyPheG1nleuArgTyrG1uThrT1leThrLeuGlnSerAspN1sGlyLeuArgProGly	630
Db	1420	GGCTTCTCATCCACATATAGAGTGAAGCGCTTGAAGTCCGATTTCTCTGGACCCGGGAC	147
QY	631	IlleProValAsnG1yGlnArgH1sGlyAsnAspPheTyrValG1yAlaLeuValThrPhe	650
Db	1480	ATCCCTGTGAACGRCATCGCCACGCTGAGACTTTGGCATCAGGACCCAGATGACTTTC	153
QY	651	SerCyAspSerG1YTyThrLeuSerAspArgLysProLeuG1uCyGAluProAsnPhe	670
Db	1540	AGCTGTGACCCGGGGTACACATTAAGTACGACAGACCCCTGCTGTGAAGGAACAC	159
QY	671	GlnTPSerArgAlaLeuProSerCyGAluAlaLeuCyGAluPhe1leGlnLysSer	690
Db	1600	CAGTGAACAACAGCCCTTGCCGACGAGCGCTTATATGAGAGGCTACATCAAGAGAG	165
QY	691	SerGlyThh1leuSerProGlyPheProAspPheTyrProAsnAsnLeuAsnCyThr	710
Db	1660	AGTGAACAGTCTTCTCTCGGGTTCCAGATTTTATCCAAATCTCTTAAACGACAG	1715
QY	711	Thr1le1leG1uThSerH1sG1yLysG1yAlaPhePheThrPheN1sThPheH1sleu	730
Db	1720	TGACACATTTGAAGTGTCTCATGGGAAAGAGTTAAATGATCTTACACACTTTCATCTT	1779
QY	731	G1uSerG1yH1sAspTyrLeuLeu1leThrG1uAsnG1ySerPheThGlnProLeuArg	750
Db	1780	GAGATGTCACAGACTATTTACTATCAACAGAGATGGAATTTTCCAGACCCGCTGCC	1838
QY	751	GlnLeuThrG1ySerArgLeuProAlaPro1leSerAlaG1yLeuTyrG1yAsnPheThr	770
Db	1840	AGGCTCACCGGGTGGGTGTCTCCATACGATCAAGCGAGGCTGTGGAACTTCACT	1899
QY	771	AlaGlnValArgPhe1leSerAspPheSerWetSerTyrG1uGlyPheAsn1leThrPhe	790
Db	1900	GCCACGCTTCGGTTATATACAGACTTTCATTTGTAACGAGGCTTCAATATCACATTT	1959
QY	791	SerGlyTyrAspLeuGlnProCyGlnGlnProGlnValProAlaTyrSer1leArgLys	810
Db	1960	TCAAGATATGACCTGGAGACCATGATGATCTTGAAGTCCCTGCTTCAGCGGAAGATT	2019
QY	811	GlyLeuGlnPheG1yAlaGlyAspThrLeuThrPheSerCyPheProGlyTyrArgLeu	830
Db	2020	GGTTTTCACTTTGGTGTGGAGACTCTCAACGTTTTCTTGCTTCCGTGGATACGTTTA	2079
QY	831	GlnGlyThrAlaG1leThrCyLeuG1yG1yAlaArgArgLeuTTPSerSerProLeu	850
Db	2080	GAAAGTGCRCAAAGCTTACCTGCTGGGGGGCGCGGTGTGTGAGATGCACCTCTG	2139
QY	851	ProArgCyValAlaG1uCyGAluAsnSerValThrG1yThrGlnGlyThrLeuLenSer	870
Db	2140	CCAAGGTGTGTGGCGGAATGTGGAGCAAGTGTCAAGAGAAATGAAGAACATTATCTTCT	2199

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Db 2200 CCAATTTTCATCCAAATATGATATACCATGATGATCTATCTAAATGAAACAGAA 2259
Qy 891 ProglYlybglYlleglnleuYlaAArgAlaPhegluleuSerGlYglYAspValleu 910
Db 2260 GCCCGCAAGGCGATCCACCTTAGAACACAGAGCTTCAGCTGTGGAAGGAAATCTCTA 2319
Qy 911 LysValTYrAspGlyAAsnAsnSerAlaArgleuGlYValPheSerHisSerGlu 930
Db 2320 AAGGATATATGATGAAAAAGACAGATTCTCAGCTCCACGTCGAGCGACGTTCAAAAAATGAA 2379
Qy 931 MetserGlyValThrLeuAsnSerThrsSerSerleuThrPleuAspPheIleThrAsp 950
Db 2380 CTCTGGGGCTGATCCTTAACAGACATCCAAATCCTTGCTAGAGTTCAACACCAAT 2439
Qy 951 AlaIleuAnthrSerLySgLYPhegluleuHiSpheserSerPhegluleuIleLySg 970
Db 2440 GGATCTGACCGACCAAGGTTTTCACTCACTATACAGTTTGAATCTGTAATAATGT 2499
Qy 971 GluAspProglYThrProLySphesGlyTYrLyValHisAspGluGlyHisPheAlaGly 990
Db 2500 GAGGATCCGGGATCCTTAACCTACGACTATAGATCCGTGATGAAAGCCACTTAAACGAC 2559
Qy 991 SerSerValSerPheSerCyAspProglYTYrSerleuAArgLYSerGlYgluleu 1010
Db 2560 ACTGATAGTTCTGATCAGTTGACACCGGGGATACGCGATGCGACATGCGACAAACCTGACC 2619
Qy 1011 CysleuSerGlygluAArgArgThrTrpAspArgProleuProthrCysValAlaGluCys 1030
Db 2620 TGTGTGATGAGACAGAGAGTGTGGGACAAACCACTGCTGTCATGCGGAAATGT 2679
Qy 1031 GlyLyThrValAArgGlygluValSerGlygluValleuSerProglYTYrProAlaPro 1050
Db 2680 GGTGTGATGATTCATGACGACCAATCAGACGAATATGTCCCTGGCTATCCAGCTCG 2739
Qy 1051 TYrGluHisAsnleuAsnCySleTrpThrIleGluAlaGluAlaGlyCySThrIleGly 1070
Db 2740 TATACAAACAACCTCCACTGACCTCGATTTATAGAGCAGACCAAGAAACCACTTAGC 2799
Qy 1071 LeuHiSphleuValPheAspThrGluGluValHisAspValleuAArgIleTrpAspGly 1090
Db 2800 CTCCATTTTCATGTTTTCGACACGAGATGCTCAGCATCTCAAGAGTCTGGGACCGG 2859
Qy 1091 ProAlaGluSerGlyValleuLeuLySgluleuSerGlyProAlaIleuProLyAspLeu 1110
Db 2860 CCGGTGACATGACATCTCTGTAAGAGTGGAGTGCCTCCGCTTCGGAGACATC 2919
Qy 1111 HisSerThrPheAsnSerValValleuGlnPheSerThrAspPheThrSerLySglu 1130
Db 2920 CACAGCACTTCAACTACTACCTCGATTCAGACGACGACTTCTTATACAGCAAGCT 2979
Qy 1131 GlyPheAlaIleGlnPheSerValSerThrAlaThrSerCyAsnAspProglYIlePro 1150
Db 2980 GGGCTTCTCATCCAGTTCTCCACTCAATTCAGCCACCTGTAACGATCCAGATATGCC 3039
Qy 1151 GluAsnGlySerAArgSerGlyAspSerTrpGluAlaGlyAspSerThrValPheGluCys 1170
Db 3040 CAAATATGACACCCGCTATGAGACAGCAGAGAGCTGAGACACCGTTCACATTCACAGGT 3099
Qy 1171 AspProglYTYrAlaLeuGlnGlySerAlaIleSerCySValAlaIleGluAsnArg 1190
Db 3100 GACCTGGCTATACGCTCCAGAGACAGCAAGCAAAATCCTGTGTGACGACTAAATACCGG 3159
Qy 1191 PhePheTrpGlnProSerProProThrCysAlleAlaProCySgLYglYAspLeuThrGly 1210
Db 3160 TTCTTTTGGCAACAGACCTCTCAATGACATAGCTGTGTGAGGAGAACTGACGCGG 3219
Qy 1211 ProserGlyValIleleuSerProAsnThrProgluProLyrrProProglYlyGluCys 1230
Db 3220 CCACAGAGGTATATTTGTTCACCAACATACCAAGCGGATCTCTCGGGAAGGAATGT 3279
Qy 1231 AspTrpLySValThrValSerProAspTrpAlaIleAlaLeuValPheAsnIlePheAsn 1250
Db 1250
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Db 3280 GACTGAGAGTAAAAAGTGAACCCGCACTTGTCTACCTGCTATATTCAAAGTTTCAAC 3339
Qy 1251 LeuGluProglYTYrAspPheleuHisIleTyTrpAspGlyAArgAspSerleuSerProleu 1270
Db 3340 ATGAGAGCCAGCTATGACTTCTTACATATATAGAGGGAAGATTCACAGCCCTCTC 3399
Qy 1271 IleGlySerPheTyrgLYSerGlnleuProglYArgIleGluSerSerAsnSerleu 1290
Db 3400 ATTGGAGATTACAGGCTCTCAGGCCCCAGAAAGAAATAGAGATACCGGAAACAGCTG 3459
Qy 1291 PheleuAlaPheArgSerAspAlaSerValSerAsnAlaGlyPheValIleAspTrpThr 1310
Db 3460 TTCTGGCATTTCCGATGATAGCTCTCGTGGGCTTTCAGAGTTCCGCAATGAAATTTAAA 3519
Qy 1311 GluAsnProArgGluSerCySPhAspProglYSerIleLySAsnGlyThrArgValGly 1330
Db 3520 GAGAAACACAGGAGAGCTGTTTGGACCGAAATATATGAAATGAGACAAAGATTGA 3579
Qy 1331 SerAspLeuLySAsnGlySerSerValThrTYrTYrCySHisGlyGlyTYrGluValGlu 1350
Db 3580 ACAGACTTCAAGCTTGCTGCTCCACATCACTACAGATGACTGCTGCTATTAAGATCTT 3639
Qy 1351 GlyThrSerThrleuSerCySleleuGlyProAspGlyLySProValTrpAsnAspPro 1370
Db 3640 GACCCCTCATCTACACTGCTGTGATTTGGGCTGATGGGAAACCTCTCGGACCAAGTG 3699
Qy 1371 ArgProValCySThrAlaProCySgLYglYgluInTyValGlySerAspGlyValleu 1390
Db 3700 CTGCCCCCTGCAATGCTCCCTGTGGAGGCGACATACCGGATGAGAAAGGGTGTGTTTA 3759
Qy 1391 SerProAsnTYrProGluAsnTYrThrSerGlyGlnIleCysleuTYrPheValThrVal 1410
Db 3760 TCACCAACTACCCCTCAATTTACACAGCTGTGTAAATATGCTCTTTCATCATACGGTA 3819
Qy 1411 ProLySAspTYrValPheglYgluPheAlaPhePheHisThrAlaIleuAsnAspVal 1430
Db 3820 CCAAGGAATTCGATGCTTGTGACAGATTTGCCATTTCCAGACGCTGAAATGATTTG 3879
Qy 1431 ValGluValHisAspGlyHisSerGlnHisSerArgleuLeuSerSerleuSerGlySer 1450
Db 3880 GCAGAATTAATTTGATGAAACCATGCAACAGCCAGACTTCTCACCTCACTCCGGGCT 3939
Qy 1451 HisThrGlyGluSerleuProleuAlaThrSerAsnGlnValleuIleLySPheserAla 1470
Db 3940 CACTCAGGGAATATGCTTCCTTGGCTTACATCAATCAATTCGCTCCGATTAAGTGA 3999
Qy 1471 LysGlyleuAlaProAlaArgGlyPheHisPheValTYrGlnAlaValProArgThrSer 1490
Db 4000 AAGAGGGGTGCTGCTGCGCGGCTTCACCTGCTGATCAAGCTGTTCCTCGTACAGT 4059
Qy 1491 AlaThrGlnCySserSerValProGluProArgTYrGlyAspGleuGlySerAspPhe 1510
Db 4060 GACACCCCAATGCAAGCTGTGCTCCCGACCCAGAAATACGAAAGAAATGTGTTCTGAAGTT 4119
Qy 1511 SerValGlyAlaIleValAArgPheGluCyAsnSerGlyTYrAlaLeuGlnGlySerPro 1530
Db 4120 TCTCCGAGCTCATCGTCCGATTCGATTCACACCCGGAATACCTGCTTCAAGGTTCCAGC 4179
Qy 1531 GluIleGluCysleuProValProglYAlaIleuAlaGlnTrpAsnValSerAlaProThr 1550
Db 4180 GCGCTCAACGCGACGTCGCGGCCCAACGCGTGGCAAGTGAACGACAGATCCGACG 4239
Qy 1551 CysValAlaProCySgLYglYAsnleuThrGluAArgArgGlyThrIleleuSerProglY 1570
Db 4240 TGTGTGTATACCTGCAATGCAATTCATCAACGAAAGAGTCAATCTGTGCTCCCGCG 4299
Qy 1571 PheProgluProTYrleuAsnSerleuAsnCySValIleTrpLySleValIleProgluGly 1590
Db 4300 TACCTTAAGCATACGAAACAACTTAAGTATATAGAAATCATATGATTAACGAGAGGC 4359
Qy 1591 AlaGlyIleGlnIleGlnAlaIleSerPheValThrGluGlnAsnTrpAspSerleuGlu 1610
Db 4360 TCGGGAATTCAGATCCAAAGTATCATGTTTGGCCAGGACGAACTGGACTCTCCCTGAG 4419
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QY 1611 ValPheAspGlyAlaAspAsnThrValThrMetLeuGlySerPheSerGlyThrThrVal 1630
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Db 4420 ATCCAGATGCTGGGGATGTGACCCGACAGCTGGAGAGCTTCTCAGGACCACTA 4479
QY 1631 ProAlaLeuLeuAsnSerThrSerAsnGlnLeuTyrLeuHisPheTyrSerAspIleSer 1650
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Db 4480 CCGGACATCTGTGAACAGTACTTCCAAACCACTTCAGTTCATTCCTGACATTTAGT 4539
QY 1651 ValSerAlaAlaGlyPheHisIleuGlnTyrLysThrValGlyLeuSerSerCysProGlu 1670
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Db 4540 GTGGAGCTGCTGTTTCCACCTGGAAATACAAACTGTAGGTCCTTGCTGCATGCCAAGA 4599
QY 1671 ProAlaValProSerAsnGlyValLysThrGlnGlyLysGlyTyrLeuValAsnAspValVal 1690
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Db 4600 CCAGCCTCCCGACGACAGCATCAAAATCGGAGATCGGTACATGGTAACAGACGTCTCTC 4659
QY 1691 SerPheGlnCysGlnProGlyTyrAlaLeuGlnGlyHisAlaHisIleSerCysMetPro 1710
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Db 4660 TCCTTCCAGTGTGAGCCCGGGTACACCTCGAGGGCGGTTCCCATTTCTCTGATGCCA 4719
QY 1711 GlyThrValAlaArgAlaGlyTyrAsnTyrProProProLeuCysIleAlaGlnCysGlyGlyThr 1730
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Db 4720 GGGACCTTCCGCGCTGGTGAACCTATCCGCTCCCTGTGCATTTGCAACCTGTGGAGGAGC 4779
QY 1731 ValGlnGluMetGlnGlyValIleLeuSerProGlyPheProGlyAsnTyrProSerAsn 1750
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Db 4780 CTGAGACACTTGGGTGGTGTGATCTGTAGCCCGGCTTCCAGGTTCTTACCCCAACAC 4839
QY 1751 MetAspCysSerTyrPheIleAlaLeuProValGlyPheGlyAlaHisIleGlnPheLeu 1770
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Db 4840 TTAACTGTGACCTGTGAAGATCTCATTTACCCATCGCATGTGTGACATATTCAAGTTCTCTG 4899
QY 1771 AsnPheSerThrGlnProAsnHisAspTyrIleGlnIleArgAsnGlyProTyrGlnThr 1790
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Db 4900 AATTTTCTACCGAAGCTAATCATGACTTCTTAAATTCAAATGAGACCTTACCAACCC 4959
QY 1791 SerArgMetGlnGlyArgPheSerGlySerGlnLeuProSerSerLeuLeuSerThrSer 1810
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Db 4960 AGCCCAATGTATGACAAATTTAGCGGACAGATCTCCCGCGGCGCTCGTACACACAC 5019
QY 1811 HisGlnThrThrValTyrPheHisSerAspHisSerGlnAsnArgProGlyPheIleLeu 1830
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Db 5020 CATGAACCTCATCCACTTTTAAATGTGACCATTTGGAAAAACCGGAAAGATTTAAACTT 5079
QY 1831 GlnTyrGlnAlaTyrGlnLeuGlnGlnCysProAspProGlnProPheAlaAsnGlyIle 1850
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Db 5080 GCTTACCAAGCCTATGATTAACAGAACTGTCCAGATCCACCCCATTTCAAGATGGGTAC 5139
QY 1851 ValArgGlyAlaGlyTyrAsnValGlyGlnSerValThrPheGlnCysLeuProGlyTyr 1870
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Db 5140 ATATATCAATCTGGATTAACAGCTGGGGCAATCAGTATCTTTCCAGATGTTATCTGGGTAC 5199
QY 1871 GlnLeuThrGlyHisProValIleuThrCysGlnHisGlyThrAsnArgAsnThrPheHis 1890
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Db 5200 ATTCTAATAGCCATCTGTCTCTCATCTTGTACAGATGGATCAACGAAACTGGAATCAC 5259
QY 1891 ProLeuProLysCysGlnValProCysGlyGlyAsnIleThrSerSerAsnGlyThrVal 1910
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Db 5260 CCTTTTCCAAAGATGATGCCCTGTGTGGGTACAACTGAATCTTCAGAACGGCAACATC 5319
QY 1911 TyrSerProGlyPheProSerProTyrSerSerSerGlnAspCysValThrPheIleThr 1930
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Db 5320 TACTCCCTGTGGCTTCTCTGATGATGATCCGATCTCGAAGACTGATTTGGCTCATACAG 5379
QY 1931 ValProIleGlyHisGlyValAlaArgLeuAsnLeuSerLeuLeuGlnThrGlnProSerGly 1950
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Db 5380 GTGCTCCAGGGGAGGAGTTAAACATCACTTCACTCTTTCAGACGGAACCTGTCAAC 5439
QY 1951 AspPheIleThrIleTyrAspGlyProGlnGlnThrAlaProArgLeuGlyValPheThr 1970
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Db 5440 GATTACATTGCTGTTGGAGCGTCCGATCAGAACTCACCCAGCTGGAGTTTTCAGT 5499

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QY 1971 ArgSerMetAlaLysThrValGlnSerSerSerAsnGlnValLeuLeuLysPheHis 1990
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Db 5500 GGCAACACAGCCTCTCAAAACGGGCTATGATCTCACCAACCAAGTCTGTCAAGTTCCAC 5559
QY 1991 ArgAspAlaAlaThrGlyGlyIlePheAlaIleAlaPheSerAlaTyrProLeuThrLys 2010
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Db 5560 AGGACATTTCAATGAGAGCTTCTTGTCTCAATTTCCAGCATTTCAAGCTCAAGAA 5619
QY 2011 CysProProProThrIleLeuProAsnAlaGlnValValThrGlnAsnGlnGlnPheAsn 2030
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Db 5620 TGTCAACTCCCGACAGGTTTCCAGGAGAAATCTTACTGAGGATGATGATTTTCGAG 5679
QY 2031 IleGlyAspIleValArgTyrArgCysLeuProGlyPheThrLeuValGlyAsnGlnIle 2050
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Db 5680 ATAGAGATTTGTGAAATGATCAAGTCCACCCCGGGTACACTTGTGGGAGCCGACAT 5739
QY 2051 LeuThrCysLeuLeuGlyTyrThrLeuGlnPheGlnGlyProProProIleCysGlnVal 2070
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Db 5740 CTGACTTGCAGACTCATTTCCAGTGTGAGGTTGAGGTTCTTCCCAACATGTAAAGCA 5799
QY 2071 HisCysProThrAsnGlnLeuLeuThrAspSerThrGlyValIleLeuSerGlnSerTyr 2090
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Db 5800 CATGCCCGAATGAATGAAGTCCGAGCTGGATCATGGAGATCATTTCTCAGTCCAGGAT 5859
QY 2091 ProGlySerTyrProGlnPheGlnThrCysSerTyrPheValArgValGlnProAspTyr 2110
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Db 5860 CCGGATTAATTTTAATCTCCAGACTGCTCTTGAGATTAATTAAGGGAACCAAACTAC 5919
QY 2111 AsnIleSerLeuThrValGlnTyrPheLeuSerGlnLysGlnTyrAspGlnPheGlnIle 2130
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Db 5920 AACATTACATCTTGTGTGACACATTTCAAGTGAAGAAACGATTGATGACCTGGAAATG 5979
QY 2131 PheAspGlyProSerGlyGlnSerProLeuLeuLysAlaLeuSerGlyAsnTyrSerAla 2150
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Db 5980 TTTGATGTTCTTCTGGGCAAGTCTCTGTGATGATTAAGTGAAGGATCATCTGAA 6039
QY 2151 ProLeuIleValThrSerSerSerAsnSerValTyrLeuAsnGlyTyrPheSerAspHisAla 2170
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Db 6040 CAATCAATTTTAAACAGAGAGTATGATTAATTCCTCGTGTCCAGTCAACCATGCC 6099
QY 2171 TyrAsnArgLysGlyPheLysIleArgTyrSerAlaProTyrCysSerLeuProArgAla 2190
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Db 6100 AACAGTAGAAGAGATTCAGATTCGATGACACACTTCTCAGTTTACACCAACCC 6159
QY 2191 ProLeuHisGlyPheIleLeuGlyGlnThrSerThrGlnProGlyGlySerIleHisPhe 2210
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Db 6160 CTGAAGAAATGGGGTATTTTAAACAGACTCCAGAGCGGTTGGAAACCAAGTCAATTAT 6219
QY 2211 GlyCysAsnAlaGlyTyrArgLeuValGlyHisSerMetAlaIleCysThrArgHisPro 2230
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Db 6220 TTTTGCAGCCTGTATACCAATGTGTGGCCACAGCAATGCACCTGTAGCGAAACCA 6279
QY 2231 GlnGlyTyrHisLeuTyrPheSerGlnAlaIleProLeuCysGlnAlaLeuSerCysGlyLeu 2250
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Db 6280 CTGGCATGTATCCAGTGGGACTCCCTCAGCCACTGTGACAGGCTGTGTCTGGAAATC 6339
QY 2251 ProGlnAlaProLysAsnGlyMetValPheGlyLysGlnTyrThrValGlyThrLysAla 2270
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Db 6340 CCAAGATCCCGGAGAAACGGTTCATTTAACCGGAAACCAAGTTCATTGGAACAGTAAAGTG 6399
QY 2271 ValTyrSerCysSerGlnGlyTyrHisLeuGlnAlaGlyAlaGlnAlaThrAlaGlnCys 2290
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Db 6400 GTCTATGAATGTATGAGGGCTTCAAGCTTGAATCCAGCAGCAACAGCAACGCGTGTGT 6459
QY 2291 LeuAspThrGlyLeuTyrPheSerAsnArgAsnValProProGlnCysValProValThrCys 2310
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Db 6460 CAAGAGATGGCTGTGTGACTTAAACAGGGGAAACCCGCCAGTGAAGCGGCTGTGC 6519
QY 2311 ProAspValSerSerIleSerValGlnHisGlyArgTyrArgGlnLeuIlePheGlnThrGln 2330
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Db 6520 CCAAGCATTAAGCTCAGCTCTCAAGAACATGTATCTGAGGCTGTGATTCAGGATCTTGG 6579
QY 2331 TyrGlnPheGlnAlaGlnLeuMetLeuIleCysAspProGlyTyrTyrTyrThrGlnGln 2350

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Db	6580	AATGATGATCGGTGCTCAAGATATGCTGAGCTGCAGTCTCGTATCTATTGAAGAGCTGC	6639
Qy	2351	ArgValIleAcSGySGInIaAsnGlyuSerPseLeuGlyAAsPserThrProThrCys	2370
Db	6640	AGGCTCTCGCGGTGCGACGCCAATGGACCGTGGAAACATAGAGATGAGAGGCCAAGCTGT	6659
Qy	2371	ArgIleIleSerCySGIyGluLeuProIleProProAsnGlyIhAargIleGlyThrLeu	2390
Db	6700	CGAGTTATCTCGTGTGGAAAGCTTTCTTTCTCCCAATGGCAACAGATTGGAAAGCTGT	6759
Qy	2391	SerValThrGlyValaThrAlaIlePheSerCyAAsnSerGlyThrThrLeuValGlySer	2410
Db	6760	ACAGTTTATGGGGCCACAGCTATATTTACGTGCACACCGGCTCAGCTTGTTGGGGCT	6819
Qy	2411	ArgValArgGlyIuCyMeMetIaAsnGlyLeuThrPseGlySerGlyValaIArgCyALeuAla	2430
Db	6820	CATGTCAAGAGTCTGTGGCAATGGGCTCTGGAGCGGCAGCAAACTCGATGCTGGCT	6879
Qy	2431	GlyIhAcSGyGlyThrProGluProIleValaAsnGlyIhIleAsnGlyGluAAsnThrSer	2450
Db	6880	GGCCACTCGGGTCCCCAGACCCGATTTGAAAGGTGCATTAAGTGAGATGGCTTCAGT	6939
Qy	2451	ThrArgGlySerValValThrGlnCyAAsnAlaGlyPheAlaGluIleGlyMeSerVal	2470
Db	6940	TACAGAGACAGGGGTGTACACAGTCAATCTGGTTTCGGGCTTGAGGAATCTCGTG	6999
Qy	2471	ArgIleCySGInIaAsnPhIleThrPseGlyIuSerThrProPheCyAValProIleThr	2490
Db	7000	AGGATATGCTCTGCAGAACCAACAAAGTGGTCTGGACAAAGCCTGTGTGTCCATCACA	7059
Qy	2491	CySGIyIhAcProGlyAAsnProValaAsnGlyLeuThrGlnGlyAAsnGlnPheAAsnLeuAAsn	2510
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 DEFINITION Sequence 3 from Patent WO0210199.
 ACCESSION AX374893
 VERSION AX374893.1 GI:19169788
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 ORGANISM Rattus rattus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE 1
 AUTHORS Welcher, A. A. and Elliott, G. S.
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 JOURNAL Patent: WO 0210199-A 3 07-FEB-2002;
 Amgen Inc. (US)
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ORIGIN

Alignment Scores:

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US-10-016-248-2 (1-3104) x AX374893 (1-12525)

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Dp	5113	TGGCTGGACATGCTCTCCAGAGCATGAGTGTACATCACTTCACTTCTGTGACACT	5172
Oy	1947	GluProSerGlyAepPheIleThrIleTrpAepGlyProGlnGlnThrAlaProArgLeu	1966
Dp	5173	GAGCGCTGAATGACTACATCGCTGTGGATGGTCTGTGACAGAACTCCGCTACGCTC	5232
Oy	1967	GlyValPheTrpArgSerMetAlaIleValThrValGlnSerSerSerAsnGlyValIleu	1986
Dp	5233	GGGCTCTTCAGTGAAACACATGCTCCCTCGAGACAGATACACTCACAACCAAGTCTTG	5292
Oy	1987	LeuTyPheH1eAArgAspAlaAlaThrGlyGlyIlePheAlaIleAlaPheSerAlaTy	2006
Dp	5293	CTCAAAATTCACAGAGGATTCCTCCAAATGGAAGCTTCTTGTCCCAATTTTCATGACATT	5352
Oy	2007	ProLeuThrTyCyPProProProThrIleLeuProAenAlaGlyValValThrGluAen	2026
Dp	5353	CAACTGAAAGAGTGCCTCCCTCTCCAGATGCGCGAGCTGCATCTGCTTACAGAAAT	5412
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Dp	5413	GAGAGCTTGAATATGGGAGCTTGTGAATAGTACAGATGCATTCAGGATACACCTGTG	5472
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Oy	2067	IleCyGlyValH1eCyPProThrAenGluLeuLeuThrAepSerThrGlyValIleLeu	2086
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Dp	5773	AACCACTAGAACGTCCAAATTTTACACGAGAAAGTAAACAATCTGATCTCCGTGGTCC	5832
Oy	2167	SerAepH1eAlaTyPAsnAlaGlyGlyPheTyPleAArgTyPserAlaProTyCySer	2186
Dp	5833	ACAAGTATCGAACAAGCAAAAGAAAGATTCAAGATGCGTATGCAAGCTCTTACTGCAAG	5892
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Dp	5893	CTCAACCTTCACTCAAGATAGTGGCGTTTAAATAAACAAGGAGGCGCCTGGGAGG	5952
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Dp	5953	AAGGTGACGATTTTCTGCAGCCTGGATATGATGATTTGGCACAAGCAAGCAACCTGC	6012
Oy	2227	ThrArgH1eProGlnGlyTyPTh1eLeuTyPserGlnAlaIleProLeuCyGlyAlaIleu	2246
Dp	6013	AGCGGAAACCAAGTGGGCGGTGTACACAGTGGAGCTGATGGGACCGGCTTTGCCAAGCTGTG	6072
Oy	2247	SerCyGlyLeuProGlnAlaProTyAenGlnMetValPheGlyGlyGlyTyPThrVal	2266

Db	6073	TCCTGTGGAATTCAGAGGCTCCAGGAAATGGCTCGTTCCACAGGCAATGAGTTACCTTA	6132
Oy	2267	GLYThrValAlaValTYrSerCysSerGluGlyTYrHisLeuGlnAlaGlyAlaGluAla	2286
Db	6133	GACAGTAAGAAGCATTTATGATGATGTAATGAAGAGGCTTCAAGCTGCAATGCCAGTACAGCAAGCC	6192
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Db	6193	ACTCTGTGTGTCTCAAGAAATGGCTGTGTGAGCAACAGAGAAAGCCACCCAGCTGCMAA	6252
Oy	2307	ProValThrCysProAspValSerSerLeuSerValGluHisGlyArgTrpArgLeuLe	2326
Db	6253	CCGGTGGCCCTGGCCCAAGCATCGAAAGCCAGCTGTCAAGACAGCGTCTGTGAGGCTGATT	6312
Oy	2327	PheGluThrGlnTrpGlnPheGlnAlaGlnLeuMetLeuLeuCysAspProGlyTYrTYr	2346
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Db	6373	TTGCAAGGTCACAGAGGCTGTGTGACAGTGCACCAAGCTGGAACTGTGAACACTGAGGAGAGC	6432
Oy	2367	ThrProThrCysAspGluIleIleSerCysGlyGluLeuProProAsnGlnHisArg	2386
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Db	6493	ATAGGAGCGCTCATATGATATGAGGCCACCGGCATCTTTACTCTGCATATACCGGCTACACA	6552
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Db	6553	CTTTAGAGCTCCCATGTCCTGGAGATGCTTGGCCAAATGGTCTGTGAGCCGATCGAAACA	6612
Oy	2427	ArgCysLeuAlaGlyHisCysGlyThrProGluProIleValAsnGlnHisIleAsnGly	2446
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Oy	2447	GluAsnTrpSerTYrArgGlySerValValTYrGlnCysAsnAlaGlyPheArgLeuLe	2466
Db	6673	GATGGCTTCAAGCTACAGGACACAGAGTGTCTTACCAATGCAACCTGGGTTTCACTGTGA	6732
Oy	2467	GlyMetSerValArgIleCysGlnGlnAspHisHisTrpSerGlyLysThrProPheCys	2486
Db	6733	GGCAGCGTGTGAGAGATTGGCTGTCAGACACAAAGTGTCCGGGCGAGACCCCGTTTGC	6792
Oy	2487	ValProIleThrCysGlyHisLeuProGlyAsnProValAsnGlyLeuThrGlnGlyAsnGln	2506
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Oy	2507	PheAsnLeuAsnAspValLysPheValCysAsnProGlyTYrMetAlaGlnGlyAla	2526
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Oy	2567	ProHisArgPheAspPheGlyThrThrValSerTYrArgCysAsnHisGlyPheTYrLeu	2586
Db	7033	CCACAGAGATTTCAGTATGGGACAAAGTGTATGTATCATCTGCAAGAAAGGGGTTCATCTTA	7092
Oy	2587	LeuGlyThrProValLeuSerCysGlnGlyAspGlyThrTrpAspArgProArgProGln	2606
Db	7093	CTGGGCTCTTGTGCGCTGACCTGTGATGGCAAGTGGCTGTGGGACCGCTCTTAACCAAG	7152
Oy	2607	CysLeuLeuValSerCysGlyHisProGlySerProProHisSerGlnMetSerGlyAsp	2626

Db	7153	TGCTGGCTATATCATATGTGGGCAATCCCTGGGGTCCCGGCTAAATGCTGTCTGATCGAGAA	7212
Qy	2627	SeTyrThrValGlyValValArgTyrSerCysIleGlyLeuArgThrLeuValGly	2646
Db	7213	TTGTTCATATTGGAGGCAAGCTTCAGTCACTCTCGTCAAGGGGGCCAGATTTCTCAACGC	7272
Qy	2647	AanSerThrArgMetCysGlyLeuAspArgLysIleTPThrGlySerLeuProHisCysSer	2666
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AUTHORS	1 Shimizu A., Asakawa S., Saeki T., Yamazaki S., Yamagata H., Kudo H., Minoshima S., Kondo T. and Shimizu N.		
TITLE	A novel giant gene CSMD3 encoding a protein with CUB and sushi multiple domains: a candidate gene for benign adult familial myoclonic epilepsy on human chromosome 8q23.3-q24.1		
JOURNAL	Biochem. Biophys. Res. Commun. 309 (1), 143-154 (2003)		
MEDLINE	22824680		
PUBMED	12943675		
REFERENCE	2 (bases 1 to 13040)		
AUTHORS	Shimizu N., Asakawa S. and Shimizu A.		
TITLE	Direct Submission		
JOURNAL	Submitted (11-JUL-2003) Nobuyoshi Shimizu, Keio University School of Medicine, Molecular Biology, 35 Shinanomachi, Shinjuku-ku, Tokyo 160-8582, Japan (E-mail: nshimizu@mb.med.keio.ac.jp, Tel: 81-3-3351-2370, Fax: 81-3-3351-2370)		
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TITLE	1	
JOURNAL	Shimizu, A., Asakawa, S., Sasaki, T., Yamazaki, S., Yamagata, H., Kudo, J., Mhoshima, S., Kondo, I. and Shimizu, N.	
REFERENCE	A novel giant gene CSM3D encoding a protein with CUB and sushi multiple domains: a candidate gene for benign adult familial myoclonic epilepsy on human chromosome 8q23.3-q24.1	
PMID	Biochem. Biophys. Res. Commun. 309 (1), 143-154 (2003)	
PIRAME	22824680	
PIRAME	12943675	
AUTHORS	2 (bases 1 to 13040)	
TITLE	Shimizu, N., Asakawa, S. and Shimizu, A.	
JOURNAL	Submitted (11-Jul-2003) Nobuyoshi Shimizu, Keio University School of Medicine, Molecular Biology, 35 Shinanomachi, Shinjuku-ku, Tokyo 160-8582, Japan (E-mail: nshimizu@cmb.med.keio.ac.jp, Tel:81-3-3351-2370, Fax:81-3-3351-2370)	
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ORIGIN

Alignment Scores:

Pred. No.: 0 Length: 13040
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 Best Local Similarity: 60.07% Mismatches: 665
 Query Match: 62.36% Indels: 41
 DB: 9 Gaps: 6

US-10-016-248-2 (1-3104) x AB114605 (1-13040)

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Db 6220 ACTCTTACAGCTGGAATTAATTAATGGAGACAGATATATGTTGAGATGTAGTATCTCT 6279
Qy 1693 GlnCyGluProG1YTrAlaLeuGInglYhi1A1IleG1YSerCyMetProG1YThr 1712
Db 6280 CAGTGATATAGATATCTCTTCAAGGCTCTCACTTCAATCATGATAGCAAGGACCT 6339
Qy 1713 ValArgArgTrpAenTyTrProProProLeuCyAlaAlaGlnCySglYTrhValGlu 1732
Db 6340 GTAAGAAAGATGAAATTAATCAATCCAAATTTGTTTGTAGTCAAGTGTGTGATGTCA 6399
Qy 1733 GluMetGluG1YVal1IleLeuSerProG1YpHeProG1YAsnTyTrProSerAenMetAsp 1752
Db 6400 GACTCAGTGTGTGATCTCCAGTCTGGGTTTCTGGAATACTCCACAGATTATGAT 6459
Qy 1753 CySerThrLyS1IeAlaLeuProVal1G1YpHeG1YAla1IleGlnPheLeuAenPhe 1772
Db 6460 TGCACATGACAATAATCAACCAATAGTTTGGTATCATCTCAAGTGTGTAATTT 6519
Qy 1773 SerThGluProAenhi1AspTyTr1IeGln1IeArgAsnG1YProTyTrGluThrSerArg 1792
Db 6520 TCTACAGAAACATATCATGATTTATTTGGAAGTACGAAGTGAATCCAGAAACTAGTACT 6579
Qy 1793 MetMetG1YArghPheSerG1YLeuProSerSerLeuLeuSerThrSerhi1eGlu 1812
Db 6580 GTTATGGCCGGCTAGTGTGCTCAAAATCACTTCTTATTTACGACACCACTTGA 6639
Qy 1813 ThThVal1YrThen1IleSerAspPhe1IleSerGlnAsnArgProG1YpHeLySLeuG1YTr 1832
Db 6640 ACCAGCTATATTTTCAACATGACTATTCACAAACAAACAGGTTCTATATGTATAC 6699
Qy 1833 GlnAlaTyTrGluLeuGInglYCyProAspProGluProPheAlaAenG1Y1IeValArg 1852
Db 6700 CAAGCTTATGAGTTCGAAGAGCTGCTGATCCACGCCGTTTGGAAATGTTTGTATAT 6759
Qy 1853 G1YAlaG1YTrAsnVal1G1YInSerValThrPheGlnCyAenProG1YTrGlnLeu 1872
Db 6760 GGTATATATTTCTGTGGGTCAACCATTTCAATTTGAATGTTTCCAGATACACATTA 6819
Qy 1873 ThG1Yhi1SerProVal1LeuThrCySglnhi1eG1YThAsnArgAsnTrpAspPhe1IleProLeu 1892
Db 6820 ATGGAATTCACCTCAGATGCTTTCAGAGGATCAGTGTATATGGAATCATCCACT 6879
Qy 1893 ProLySLeuGluVal1ProCysG1YAsn1IeThSerSerAenG1YThrVal1YrSer 1912

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Db      6880 CCAGGTGTGAGCTCTTTGGTGGGAATATACTGCATGAATGACCATTTATCT 6939
Qy      1913 ProGlyPheProSerProTyrSerSerSerGlnAspCysValTyrPheIleThrValPro 1932
Db      6940 CCTGGGTATTCCTGATGAATATCCAAACTTTGAAAGATGTGTTTGGCTTGTAAGAGTACC 6999
Qy      1933 IleGlyHisGlyValArgLeuAsnLeuSerLeuLeuGlnThrGluProSerGlyAspPhe 1952
Db      7000 CCGGGAATGGCATCTACATCAATTTTACTGTCTCTCAACAGAACCAATATATGATTTTC 7059
Qy      1953 IleThrIleTyrPheArgGlyProGlnGlnThrAlaProArgLeuGlyValPheThrArgSer 1972
Db      7060 ATTACTGATGTGGATGACACGACCAAAATTCACCTCAGATCGGTCACTCAGTGGCAAT 7119
Qy      1973 MetAlaIleValThrValGlnSerSerSerSerSerGlnIleLeuLeuLysPheHisArgAsp 1992
Db      7120 ACCGCTTGGATCAGTCTACAGTATCAATCTCAATCAATCTCAATCAATCTCAATGAT 7179
Qy      1993 AlaAlaThrGlyGlyIlePheAlaIleAlaPheSerAlaTyrProLeuThrLysCysPro 2012
Db      7180 TTCAACAACAGTGGCTTTTGTGCTCAGTATCAGCGCTATCAACTAAGGTTGTCCAA 7239
Qy      2013 ProProThrIleLeuProAsnAlaGluValAlaThrGluAsnGluGluPheAsnIleGly 2032
Db      7240 CCTCACCACTGTCGCCCAATGCTGAATTTTGAAGAGATGATGAATTTGAATAGGT 7299
Qy      2033 AspIleValArgTyrArgCysLeuProGlyPheThrLeuValGlyAsnGluIleLeuThr 2052
Db      7300 GATATTATAGTATCAGTGTCTTCCAGATTTACTTATGTTGATGCAATTCGATGACG 7359
Qy      2053 CysAlaIleuGlyThrTyrLeuGlnPheGluGlyProProIleCysGluValHisCys 2072
Db      7360 TGCAGATTAGAGAACACGACGACAGATGATGAGACCTCAGTTGTCAAGTGTCTGT 7419
Qy      2073 ProThrAsnGluLeuLeuThrAspSerThrGlyValIleLeuSerGlnSerTyrProGly 2092
Db      7420 CCTGCCAATGATTAACGGCTAGATTTCTACGAGTCAATATGAGCCCTGATATCCTGAC 7479
Qy      2093 SerTyrProGlnPheGlnThrCysSerTyrPheValArgValGluProAspTyrAsnIle 2112
Db      7480 AGTTAACCAATCTTCAATATGTTGTCATGAGCATGAGCATTTCACTGAGAAAGGTTATATC 7539
Qy      2113 SerLeuThrValGluTyrPheLeuSerGlnLysGlnTyrAspGluPheGluIlePheAsp 2132
Db      7540 ACCATGTTGTAGAAATCTTCCAGACAGAAAGAAATTTGATGTTCTTCAGGTGATGAT 7599
Qy      2133 GlyProSerGlyLysSerProLeuLeuValAlaLeuSerGlyAsnTyrSerAlaProLeu 2152
Db      7600 GGAACCAATATTCAAAGTCCAGTGTCTTATTCCTCAGTGGGATTTATCATCTGCTTTT 7659
Qy      2153 IleValThrSerSerSerSerSerSerValTyrLeuArgTyrPheSerSerAspHisAlaTyrAsn 2172
Db      7660 AATATTAACAAGCAATGCTCATGAAGTATTTCTTCAGTGTGACACATCATGSCAATATC 7719
Qy      2173 ArgIleGlyPheLysIleArgTyrSerAlaProTyrCysSerLeuProArgAlaProLeu 2192
Db      7720 AAAAAAGGCTTCGGAAATAGATATATAGCTTTCTACTGTAGTACACCAAAATCCCACT 7779
Qy      2193 HisGlyPheIleLeuGlnThrSerThrGlnProGlyIleSerIleHisPheGlyCys 2212
Db      7780 CATGATATATTTATCATGTCACAGACAGTGGGCACTTAACAGTGTGCTGTTGGGCTGT 7839
Qy      2213 AsnAlaGlyTyrArgLeuValGlyHisSerMetAlaIleCysThrArgHisProGlnGly 2232
Db      7840 GATCGAGGATTCGACCTTGTGGAAAAAGCAGTGTGTGCGAAGAACTTCCTATGGG 7899
Qy      2233 TyrHisLeuThrSerSerGlnAlaIleProLeuCysGlnAlaLeuSerCysGlyLeuProGlu 2252
Db      7900 TATCATGATGATGGATGGCAGTCCCTGCTGTCAAGCAATTTCTGTGGGATTCCTATA 7959
Qy      2253 AlaProLysAsnGlyMetValPheGlyLysGluTyrThrValGlyThrIleValAlaValTyr 2272
Db      7960 GCTCCAAACAATGAGGAATATCTAACACAGACTATTTGTAGGAACGGAGATTACCTAT 8019

Qy      2273 SerCysSerGlnGlyTyrHisIleLeuGlnAlaGlyValAlaThrAlaGluCysLeuAsp 2292
Db      8020 TTTTGAATGATGAGATATGATGTATCATCAAAAGAACTCATCACTGATATGSCAATCA 8079
Qy      2293 ThrGlyLeuThrSerAspAsnArgAsnValProProGlnCysValProValThrCysProAsp 2312
Db      8080 GATGAACTGGAGCATATATACAAAGACCCCTCGCTGTGTGTGTATACATGATCCCAAC 8139
Qy      2313 ValSerSerIleSerValGluHisIleArgTyrArgLeuIlePheGluThrGlnTyrGln 2332
Db      8140 ATCAATCTCTTATCTTGGACATGATGAAGATGGCGAATTGTGAAGGCTCCATATGAA 8199
Qy      2333 PheGlnAlaGlnLeuMetLeuIleCysAspProGlyTyrTyrTyrThrGlyGlnArgVal 2352
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Qy      2353 IleArgCysGlnAlaAsnGlyLysTyrPheSerLeuGlyAspSerThrProThrCysArgIle 2372
Db      8260 ATCGAATGTCTTCTAATGTATCTTGGATGGAGATGGAAGAAAGCAATATTTGCCAAAT 8319
Qy      2373 IleSerCysGlyGluLeuProIleProProAsnGlyHisArgIleGlyThrLeuSerVal 2392
Db      8320 ATTCTCTGGAGAACTACTACCTCACTCAATGGAATATGATTTGAACCTCAACTCA 8379
Qy      2393 TyrGlyAlaThrAlaIlePheSerCysAsnSerGlyTyrThrLeuValGlySerArgVal 2412
Db      8380 TATGGCTCAACAGCTATCTTATCTTACCTGGACCTGGGATTCATGCTTGTGGCTCTCT 8439
Qy      2413 ArgGluCysMetAlaAsnGlyLeuThrPheSerGlySerGlyValArgCysLeuAlaGlyHis 2432
Db      8440 AGGAATGCTTTCTCTCAGTCTTTTGAGTGAATGTGAACCAAGATGCTTACGGGTAT 8499
Qy      2433 CysGlyThrProGluProIleValAsnGlyHisIleAsnGlyGluAsnTyrSerTyrArg 2452
Db      8500 TGTGAATTCAGAACTGATGTGATGTCAAGTCATTTGAGAAATATATGATATATAGA 8559
Qy      2453 GlySerValValTyrGlnCysAsnAlaGlyPheArgLeuIleGlyMetSerValArgIle 2472
Db      8560 GACACAGTTGTATATCATATGATATATCTGTTGTGATTTGATTTGCTTCACTGAGGATA 8619
Qy      2473 CysGlnGlnAspHisHisIleTyrSerGlyLysThrProPheCysValProIleThrCysGly 2492
Db      8620 TGTCAACAGAAATCAAAATGTTGTGTGCTGCTCCATCTGTGTGCTGTTAGTGTGT 8679
Qy      2493 HisProGlyAsnProValAsnGlyLeuThrGlnGlnLysGlnPheAsnLeuAspVal 2512
Db      8680 CACCTGTGTATCCAAATTTATGAGAAACAAAGTGAATGGGTCAACTTTAATGATGTG 8739
Qy      2513 ValLysPheValCysAsnProGlyTyrMetAlaGluGlyAlaAlaArgSerGlnCysLeu 2532
Db      8740 GTAACATTTCTGATCATATGATTTGGGTATCTTATGCAAGGCGCAACAAAGGCACGTCCAG 8799
Qy      2533 AlaSerGlyGlnTyrPheSerPheMetLeuProThrCysArgIleIleAsnCysThrAspPro 2552
Db      8800 GCCAACAGACAGTGGAGCAATCTCCACATATGCAAAAGGTGCAACTGTTGATCTCT 8859
Qy      2553 GlyHisGlnGlnLysSerValArgGln-----ValHisAlaSerGlyProHisArg 2569
Db      8860 GGAATTCAGGCCAATTTCAAAAGAGAAAGTAAATAGAACATGGAAT----- 8907
Qy      2570 PheSerPheGlyThrThrValSerTyrArgCysAsnHisGlyPheTyrLeuLeuGlyThr 2589
Db      8908 TTTACTTAACGCACTGTGATATCTATAGACTGCAATCTGTGATATTTTATTTTGGATCT 8967
Qy      2590 ProValLeuSerCysGlnGlyAspGlyThrTyrPheArgProArgProGlnCysLeuLeu 2609
Db      8968 TCAAGTTTGTATGTATCAACCAATGAGCAATGGGCAAACTTTACAGATGATGATCATG 9027
Qy      2610 ValSerCysGlyHisProGlyLysProProHisSerGlnMetSerGlyAspSerTyrThr 2629
Db      9028 ATTACTGTGACACCTGGCGTTCTCTTAATGACAGTCTGTGTGCGAAGATATATCT 9087

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Oy	2630	ValGtGlyAlaValValaGlyYrSerCysValIeGlyYrValrgrThrLeuValGlyYrAsnSerThr	2649
Db	9088	TTTGGGCTACTGTTCACTTCTCTGACACAGAAAGGCTTCCCTTTTAGGCGACGTATCA	9147
Oy	2650	ArgMetCysGlyLeuAspArgLysIleTrrpThcGlySerLeuProHisCysSerGlyYrHisSer	2669
Db	9148	AGAACCTGCCAATTGAATTGGCACTTGGAGTGAGTACAACTCATCTATTCTTCAGGTGATGCT	9207
Oy	2670	ValGlyValCysGlyYrAspProGlyYrIleProAlaHisGlyYrIleArgLeuGlyYrAspSerPhe	2689
Db	9208	ACTGGGACATGTGGCGCATCCACAGTACATCCCGGCATGAGCTCTAGACACAGAAACAATTTCC	9267
Oy	2690	AspProGlyYrValIleMetArgPheSerCysGlyLysIleGlyHisValIleuValArgGlyYrSerSer	2709
Db	9268	AGAACTAAATAACTGTAACGTTAGCTTGTAATCTGGTATACATCTTCACTGCTCAGAA	9327
Oy	2710	GluArgThrCysGlnAlaAsnGlySerTrrpSerGlySerGlnProGluCysGlyValIle	2729
Db	9328	GAAAGAACATGTTTAGCTTAATGCGAGTTGGACCCGGAAGCGACCGACAGTGTCCAAAGCTGTG	9387
Oy	2730	SerCysGlyYrAspProGlyYrHisProSerAspAlaArgValValPheSerAspGlyLeuVal	2749
Db	9388	CAGTGTGGTAAACCAAGAACACACAGCAATGGAAAGTCTTCGGAATTGATGGACAACA	9447
Oy	2750	PheSerSerSerIleValYrGluCysArgGluGlyYrYrYrAlaThrGlyLeuLeuSer	2769
Db	9448	TTTTCTAGTTCAGTCATTAATTATCTCTGATGAGGAGGATACATCTTTGTGACCTTCAGTT	9507
Oy	2770	ArgHisCysSerValAsnGlyYrThrTrrpThcGlySerAspProGluCysLeuValIleAsn	2789
Db	9508	AGACAGTGCACACAGCCAAATGAAACATGTGCTGGAACTTACTTAATCTTAACATTAATCAGT	9567
Oy	2790	CysGlyYrAspProGlyYrIleProAlaAsnGlyLeuArgLeuGlyYrAspPheArgYrAsn	2809
Db	9568	TGTGAGAGCCACAGGATATCCAGCCAAATGACATGATGAGATGATATATGTGCTTGA	9627
Oy	2810	LysThrValThrYrGlnCysValProGlyYrMetMetGluSerHisArgValSerVal	2829
Db	9628	CAAAATGTTCTTACATGTGTCACACAGGCTACACGATGAAATTGAATGGCTCCAGATTC	9687
Oy	2830	LeuSerCysThrLysAspArgThrTrrpAsnGlyYrHisLysProValCysLysAlaLeuMet	2849
Db	9688	AGGACTTGTACAAATTAATGACACATCGACGTGAGTAATGCCAACTTTAAGCTGTTAAC	9747
Oy	2850	CysLysProProLeuLysIleProAlaAsnGlyLysValValGlySerAspPheMetTrrpGly	2869
Db	9748	TGCCCACTCTCCGCCACAGATCTTAATGAAGAAAGCTGGAAGGAACAATTTTCAGCTGGGCG	9807
Oy	2870	SerSerValThrYrAlaCysLeuGluGlyYrYrGlnLeuSerLeuProAlaValPheThr	2889
Db	9808	TTTATGTATTAAGCTACATCTGTTCTCCAGAGCTATAGCATTCCTTCCCTGCTGTTTGACC	9867
Oy	2890	CysGluGlyYrAsnGlySerTrrpThcGlyGluLeuProGlnCysPheProValPheCysGly	2909
Db	9868	TGTCTTAGGAATGAGTACTGGAGTGGTGAATGACCGACGTCTTAACAAAGTTTGTGGT	9927
Oy	2910	AspProGlyYrValProSerArgGlyYrArgGlyLysAspArgGlyPheSerYrArgSerSer	2929
Db	9928	GACCTGTGTAACCTGCCCAAGAAAAGAGAGACGAAAGCTTTATATACACACTAGAG	9987
Oy	2930	ValSerPheSerCysHisProProLeuValIleuValGlySerProArgArgPheCysGln	2949
Db	9988	GTTTCATTTCAAGCTCAATTTTCTTTCATATTAATGAGGATCAAGACCAACAATAATGCAA	1004
Oy	2950	SerAspGlyYrThrTrrpSerGlyYrThcGlnProSerCysIleAspProThrLeuThrThrCys	2969
Db	10048	GCAATGGCACTTGAAGTGGTTCATCACTCATGCATAGAGCCTTACCAAACTCTTGT	10107
Oy	2970	AlaAspProGlyYrValProGlnPheGlyYrIleGlnHisAsnSerGlnGlyYrGlnValGly	2989
Db	10108	GAAAACCCAGGTGTGCTCCGCGACAGATCTCAGAAACAATACATTCCGATTTTCAAGTAGGA	1016
Oy	2990	SerThrValLeuPheArgCysGlnLysGlyYrYrLeuLeuGlnGlySerThrYrArgThr	3009

Db		10168	AGTCTTTACAGTTCCTCCATTCGAAAAAAGACACCCTTCCAAAGGTCTCAACAAGCACC	10227
Oy		3010	CysLeuProAsnLeuThrTPDSerGlyThrPheProAlapCyValProHisHisCySerG	3029
Db		10228	TGCCTCCCTGATCTACGTGAAGTGGAATTCAACCTGTAATGATACCCCCAACACTGTAAA	10287
Oy		3030	GlnProGluInhrProThrHISalaAenValGLYAlaLeuAspLeuProSerMetGlyTYR	3049
Db		10288	CAGCGACAAACCTCCTGCTCATGCAAAATGTCGTAGGAGATGGACCTTCATCTCATVGGTAT	10347
Oy		3050	ThrIeuIle 3052 	
Db		10348	ACACTGATT 10356	
RESULT 10				
LOCUS	ABI14604	13148 bp	mRNA	linear PRI 29-AUG-2003
DEFINITION	Homo sapiens mRNA for CSMD3 protein isoform 1, transcript variant			
ACCESSION	ABI14604			
VERSION	ABI14604.1	GI:34330130		
KEYWORDS				
SOURCE				
ORGANISM	Homo sapiens (human)			
REFERENCE	Homo sapiens			
AUTHORS	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
TITLE	Shimizu A., Asakawa S., Sasaki T., Yamazaki S., Yamagata H., Kudo H., Minohima S., Kondo I. and Shimizu N. A novel giant gene CSMD3 encoding a protein with CUB and sushi multiple domains: a candidate gene for benign adult familial myoclonic epilepsy on human chromosome 8q23.3-q24.1 Biochem. Biophys. Res. Commun. 309 (1), 143-154 (2003)			
JOURNAL	22824680			
MEDLINE	12943675			
PUBMED	2 (bases 1 to 13148) Shimizu N., Asakawa S. and Shimizu A. Direct Submision Submitted (11-JUL-2003) Nobuyoshi Shimizu, Keio University School of Medicine, Molecular Biology, 35 Shinanomachi, Shinjuku-ku, Tokyo 160-8582, Japan (E-mail:nshimizu@med.med.keio.ac.jp, Tel:81-3-3351-2370, Fax:81-3-3351-2370)			
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
FEATURES				
source				
gene				
CDS				

YANNINCIWITIIISDPGRSHLSFNDPDLSEQDFELAVAKDS PESPIIGETGAEVS
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ORIGIN

Alignment Scores:

Pred. No.: 0 Length: 13148
 Score: 10591.50 Matches: 1816
 Percent Similarity: 76.65% Conservative: 501
 Best Local Similarity: 60.07% Mismatches: 665
 Query Match: 62.36% Indels: 41
 DB: 9 Gaps: 6

US-10-016-248-2 (1-3104) x AB114604 (1-13148)

QY 36 ValIyLeuGlnIleuLeuLysSerArgGlyValIyLeuMePProSerLysAspAa 55
 DB 1501 GTGAAAAAGCCCTAATTAATTAATTAATTTGTTTCCAGGAAAGCAAC 1560
 QY 56 SerGlnLysSerValLeuThrGlnValIyValSerGlnGlyHisAsnMetCysPro 75
 DB 1561 AGCAACAAGTTTCTATCTTAATTAAGAGGATATTAACAAGCTTCAATTTAAGCCCA 1620
 QY 76 AspProGlyIleLeuProGlnArgGlyLysValArgLeuGlySerAspPheArgLeuGlySerSer 95

DB 1621 GATCCAGGAAACCAAAAAATGGAGAGAAATCCGATCGATTTTACCTTGATTAAC 1680
 QY 96 ValGlnPheThrCysAsnGlnGlyTyrAspLeuGlnGlySerLysArgIleThrCysMet 115
 DB 1681 GTGCAGTCTCTTGTATGATGAAATTAATGCTTACAGGGGCAAAAGCATCACTCTCA 1740
 QY 116 LysValSerAspMetCysLeuAlaIleThrSerAspPheIleArgProValCysArgAlaArgMet 135
 DB 1741 CGGATGCTGAAGTTTGTCTCTGCTGAGAGTATCAAGGCGCTGTGTGTAATGTGAAGAC 1800
 QY 136 CysAspAlaHisIleuAspArgLysProSerGlyIleIleThrSerProAsnPheProIleGln 155
 DB 1801 TGTGGCTCAATCTTCAAGACCAAGATGTTACCTTACATCTCCCACTTTCCTTCAG 1860
 QY 156 TyrAspAsnAsnAlaHisCysValIleThrIleIleThrAlaIleuAsnProSerLysValIle 175
 DB 1861 TATGACAGCAATGCACAATGTCTGTGGTCATCAAGCAGCATGAATCAATAATAGGTTATC 1920
 QY 176 LysLeuAlaPheGlnGluPheAspLeuGlnIleArgGlyTyrAspThrLeuThrValGlyAsp 195
 DB 1921 CAGATTAATTTGAAGAAATTTGATCTGGAGATGGCTATGATACCTTGACATTTGCCAT 1980
 QY 196 GLYGLYGLNAspGlyAspGlnLysThrValLeuTyrMetSerGlnAsnAlaCysSerAsp 215
 DB 1981 GGGGGGAAAGTTGAGATCTTACAGACATGCTCCCAAGT----- 2019
 QY 216 SerProHisThrProGlySerArgIleProGlu-----SerMetSerGlyAspIle 232
 DB 2020 -----CTGACTGGAAGCTTTGTCTACAGACTGATAGTACGATAGTACCAATG 2070
 QY 233 TrpArgGlnLysTrpThrValLeuGluIleCysArgAspIleSerSerAspAlaArg 252
 DB 2071 TGGCTGCACCTTCAACG-----GACCAAGT 2097
 QY 253 SerGlySerValArgLysSerProLysThrSerAsnAlaValGluLeuValAlaProGly 272
 DB 2098 GTTGATCTGTTGGTTCAAGGTTAACAACA----- 2130
 QY 273 ThrGlnIleGlnGlnGlySerCysGlyAspProGlyIleProAlaTyrGlyValArgGln 292
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Qy 473 SerPheLeuCyAspAspGluGlyPheLeuGlyThrGlnGlySerGlnThrIleThrCysVal 492
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Qy 2610 ValSerCyGlyLysProGlySerProProHisIleSerGlnMetSerGlyAspSerTyThr 2629
Db 9136 ATTGACTGTGACACCTGCGCTTCTCTTAATGACAGTCTGTGTGCGGAGATATACT 9195

Qy	2630	ValG1ValAlaValAlaAngTyrSerCysIleGlyValArgThrLeuValGlyValAsnSerThr	2644
Db	9196	TTTGGGTCTACTGTTCACTATTCTCTCACAAGAAACGTTTCCTTTAGGCCAGTCATCA	9255
Qy	2650	ArgMetCysGlyLeuAspGlyIleAspTrpHisGlySerLeuProHisCysSerGlyThrSer	2669
Db	9256	AGAACCTGCCAATTGAATGGCCATTGGAGGATGACAAACCTCATTTGTTCAAGTCATCT	9315
Qy	2670	ValG1ValCysGlyValAspProGlyIleProAlaHisGlyIleArgLeuGlyValAspSerPhe	2689
Db	9316	ACTGGAGCATGTGGCCATCCAGGTACTCCGGCCATGGCTCTAGACAGAAAGCAATTTC	9375
Qy	2690	AspProGlyThrValMetArgPheSerCysGlyIleAGlyIleValLeuArgGlySerSer	2709
Db	9376	AGAACTAAAGATCTGTACGTTATGCTTGTGATCTGTTACTGTTACATCTTCAATGCTCAGAA	9435
Qy	2710	GluArgThrCysGlyIleAlaAsnGlySerTrpSerGlySerGlnProGluCysGlyValIle	2729
Db	9436	GAAGAAGAACATGTTTACTATGCAATGGCAGTTGGACCCGGAAGGACAGCCAGATGTCMAAGCTGTG	9495
Qy	2730	SerCysGlyValAsnProGlyThrProSerAspAlaArgValValPheSerAspGlyLeuVal	2749
Db	9496	CAGTGTGTTACCCAGGAAACACAGCCCAATGGGAAAGTCTTCCGANTGATGGCACAACA	9555
Qy	2750	PheSerSerSerIleValTyrGluCysArgGluGlyTyrTyrAlaHisGlyLeuLeuSer	2769
Db	9556	TTTTCTAGTTCAGTCACTTATTCTCGCATGGAGGATACATCTTTCTGGACCTTCAGTT	9615
Qy	2770	ArgHisCysSerValAsnGlyThrTrpHisGlySerAspProGluCysGlyValIleAsn	2789
Db	9616	AACACGTGCACAGCCAAATGAAACATGTGCTGGAACTTTACCTTAACCTGAACAAATATAGT	9675
Qy	2790	CysGlyAspProGlyIleProAlaAsnGlyLeuArgLeuGlyValAsnAspPheArgTyrAsn	2809
Db	9676	TGTGGAGACCCAGGTATACCAAGCCAAATGAGACTGAGATGATGATTAATGTGCTTGA	9735
Qy	2810	LeuThrValIleThrTyrGlnCysValProGlyTyrMetMetGluSerHisArgValSerVal	2829
Db	9736	CAAAATGTTTCTTAACATGTGCAGCCAGGCTACACGATGAATGAATGAGCTCCAGAAATC	9795
Qy	2830	LeuSerCysThrIlyAspArgThrTrpAsnGlyThrIlyAspProValCysIlyAlaLeuMet	2849
Db	9796	AGGACTTGTACAAATTAAATGGACATGAGGTGAGATGATGCCAATTGTAAAGCTGTTACC	9855
Qy	2850	CysIlyAspProProIleuIleProAsnGlyIlyValValGlySerAspPheMetTrpGly	2869
Db	9856	TGCCCACTCTCTCCACAGATCTTAATGGAAGCGCTGGAAGGAACAATTTGCATCGTGGCG	9915
Qy	2870	SerSerValIleThrTyrAlaCysLeuGluGlyTyrGlnLeuSerLeuProAlaValPheThr	2889
Db	9916	TTTAGTATTAGCTACATCTGTTCTCCACAGCTATAGCTATCTCTTCCCTGCTGTTTGGACC	9975
Qy	2890	CysGluGlyValAsnGlySerTrpThrGlyGluLeuProGluCysPheProValPheCysGly	2909
Db	9976	TGTGTAGGAATGGTATCCTGGAGGTGTGAAGTACCGCAGGTCTTACCAAAAGTTTGTGGT	10039
Qy	2910	AspProGlyValProSerArgGlyValArgArgGluAspArgIlyPheSerTyrArgSerSer	2929
Db	10036	GACCTGGTATACCTGCCCAAGAAAGAAAGAGCGCAAAAGCTTTATATACCGTACAG	10099
Qy	2930	ValSerPheSerCysHisAspProIleuValLeuValGlySerProArgTrpPheCysGln	2949
Db	10096	GTTCATATTACAGCTCAATTTTCTTTCATATTATGTGGGATCAAGACCAAGAAATGTCCA	10155
Qy	2950	SerAspGlyThrTrpSerGlyIleHisGlnProSerCysIleAspProThrLeuThrCys	2969
Db	10156	GCAATGTGCATTGAGGTGTATCATCCCTCACTGATATAGAGCTTACCCAAACCTCTGT	10215
Qy	2970	AlaAspProGlyValProGlnPheGlyIleGlnAlaAsnSerGlnGlyTyrGlnValGly	2989
Db	10216	GAAGAACCCAGGTGTGCTGGCGAATGATCTCAGAACATATCATTCGGATTTCAAGTAGGA	10275
Qy	2990	SerThrValLeuPheArgCysGlnIlySerGlyTyrLeuLeuGlnGlySerThrThrArgThr	3009

[illegible]

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 FALIEKPREACDPGNINMGTVGDFKGTSTTYQCDSYXILIDPSITVGLAD
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 FHFYAOVAPRTSDQSSVSEPRRGRIGSEFSAGSIVRECNNGCYLLQSTALHQS
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 ENSNGCASFEPMYDTNLKPTFAKAVRFDTLNVTCTV"

ORIGIN

Alignment Scores:

Pred. No.: 0 Length: 10944
 Score: 10552.00 Matches: 1866
 Percent Similarity: 74.08% Conservative: 435
 Best Local Similarity: 60.08% Mismatches: 565
 Query Match: 62.13% Indels: 240
 DB: 9 Gaps: 11

US-10-016-248-2 (1-3104) x AY017307 (1-10944)

QY 1 MetAlaGlyAlaProProAlaLeuLeu-----LeuProCySerLeu 15
 DB 1075 ATCGATGGACGAGAGCTCCATTCATAGGCTTAAGTGCATGAACCTCCCTCCAGTT 1134
 QY 16 IleSerAsp-----CysCysAlaSerAsnGlnArgHisSer 27
 DB 1135 ATCGATGCAAGAAATTGGCTACGACTCATTTCACTCTGACACCAACCGACGGCAA 1194
 QY 28 ValAlaValAlaGlyProSerGluLeuValIleValysGlnIleGluLeuValysSerArgGlyVal 47
 DB 1195 ---GGATTTCAGCTCAAGTCAAGTCAAGGCGATTGAGTCAAGTCAAGGAGTCT 1251
 QY 48 LysLeuMetProSerLysAspAsnSerGlnLysThrSerValLeuThrGlnValAlaGlyVal 67
 DB 1252 AAGATGCTGCCAGCAAGATGAGAACCATTAATAACTGTGCTTAGGCAAGAGAGGTGT 1311
 QY 68 SerGlnGlyHisAsnMetCysProAspProGlyIleProGluArgGlyLysArgGlyLeuGly 87
 DB 1312 GCATTGGTCTCTCAATGTGTCTAGATCTCTGGATTCCAGAAATGGTAGAAGGACAGGT 1371

QY 88 SerAspHe-----ArgLeuGlyLysSerSerValGlnPheThrCysAsnGlnGlyTyrAspLeu 106
 DB 1372 TCCGACTTCAGTGAAGGTGGTGGCAATGTACAGTTTTCATAGTGAAGCAATTAGCTGCTC 1431
 QY 107 GlnGlySerLysArgIleThrCysMetLysValSerAspMetPheAlaAlaTyrSerAsp 126
 DB 1432 CAGGAGCTTAAGAGCATCACCTGTCAAGAGATTACAGACAGCGTCCGTGGTAGTGAC 1491
 QY 127 HisArgProValCysAlaGlnAlaArgMetCysAspAlaHisLeuArgGlyProSerGlyIle 146
 DB 1492 CACAGGCGCATCTCCACAGAGCAATGTGATCCCATATCTGCGTGGCCACAGGCGGCTC 1551
 QY 147 IleThrSerProAsnProIleGlnTyrAspAsnAsnAlaHisCysValTyrPheIle 166
 DB 1552 ATTACCTCCCTTAATTATCCGTTTCATATGAAATATGACACATGTGTGTGGATATC 1611
 QY 167 ThrAlaLeuAsnProSerLysValIleLysLeuAlaPheGluGluPheAspLeuGluArg 186
 DB 1612 ACCACCAACGACCCGCAAGGTCATCAACCTTCCTTGAAGATTGAGAGTGGAGCGA 1671
 QY 187 GlyTyrAspThrLeuThrValAlaAspGlyGlyGlnAspGlyAspGlnLysThrValLeu 206
 DB 1672 GCGTATGACACCCGTGACGTTGGTGAATGCTGGGAAGGTGGAGACACAGATCGGTCTTG 1731
 QY 207 TyrMetSerGlnHisAlaCysSerAspSerProHisThrProGlySerArgIleProGlu 226
 DB 1732 TACGTG-----CTCAGCGGATCCAGTGTCTCGAC 1761
 QY 227 -----SerMetSerGlyAspIleTyrArgGlnLysThrThrValLeuGluIleCys 243
 DB 1762 CTCATTGTAGCATGAGCAACCAAGATGGCTACAT----- 1797
 QY 244 ArgAspIleSerSerSerAspAlaArgSerGlySerValArgLysSerProLysThrSer 263
 DB 1798 -----CTGCAGTCGATGATAGC----- 1815
 QY 264 AsnAlaValAlaGluLeuValAlaProGly-----ThrGluIleGluGlnGly 278
 DB 1816 -----ATTGGCTACCTGGGTGTTTAAAGCTGTTTACCAAGAAATTTGAAAGGGA 1863
 QY 279 SerCysGlyAspProGlyIleProAlaTyrGlyArgArgGluGlySerArgPheHis 298
 DB 1864 GCGTGTGGGATCTCGTAATCCCGGCTTATGGGAAGCGACGCGACAGTTCCTCAT 1923
 QY 299 GlyAspThrLeuLysPheGluCysGlnProAlaPheGluLeuValGlyGlnLysAlaIle 318
 DB 1924 GAGATACACTCACCTTGAATGCCCGCGGCTTGTAGCTGGTGGGAGAGAGATTATC 1983
 QY 319 ThrCysGlnLysAsnAsnGlnTyrPheSerAlaLysLysProGlyCysValPheSerCysPhe 338
 DB 1984 ACCGTGAGCAAGAACATACAGTGTCTGGCAACAAAGCCAGCTGTGATTTTCAATGTTTC 2043
 QY 339 PheAsnPheThrSerProSerGlyValAlaLeuSerProAsnTyrProGluAspTyrGly 358
 DB 2044 TTCAACTTTACGCGATATCTGGATTAATCTGTCAACCAATTAATCCAGAGAAATAGGG 2103
 QY 359 AsnHisLeuHisCysValTyrPheLysLeuAlaArgProGluSerArgIleHisLeuAla 378
 DB 2104 AACCAACATGAACCTGTCTGGTGAATCTCGGACGACAGAAAGTGAATTCACCTATATC 2163
 QY 379 PheAsnAspIleAspValAlaGluProGlnPheAspPheLeuValIleLysAspArgAlaThr 398
 DB 2164 TTTAATATATTGATATGTGAGCTCAATTTGACTTCTTCGCGGTCAAGAGATATAGGCAAT 2223
 QY 399 AlaGluAlaProValLeuGlyTyrPheSerGlyAsnGlnLeuProSerSerIleThrSer 418
 DB 2224 TCTGACATAACTGTCTCGGATCTTTTCTGCGCAATGAATGCTTCCAGCTGGCCAGC 2283
 QY 419 SerGlnHisValAlaArgLeuGluPheGlnThrAspHisSerThrGlyLysArgGlyPhe 438
 DB 2284 AGTGGCATATATAGTGTCTGGAATTTCACTGTGACCATTTCACTACTGACAGAGGAGTTC 2343


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Qy 439 AsnIleThrPheThrThrPheArgHisAsnGluCysProAspProGlyValProValAsn 458
Db 2344 AACATCATCTTAAACCAACATTTGGTGCAGATGATGATCCATGATCTGGGATTTCTTAATAAC 2403
Qy 459 GlyValArgPheGlyAspSerLeuGlnLeuGlySerSerIleSerPheLeuCysAspGlu 478
Db 2404 GGACACACGTTTGGTGAACGGTTTCTACTCGGAGACGTTTCTTTTCCATGATGAT 2463
Qy 479 GlyPheLeuGlyThrGlnGlySerGluThrIleThrCysValLeuValGluGlySerVal 498
Db 2464 GCGTTTGTCAAGACCCAGAGATCCAGATCTTACTGATCTGCAATGCAAGAGGGAACGCTG 2523
Qy 499 ValTrpAsnSerValValLeuArgCysGluValProCysGlyGlyIleLeuThrSerPro 518
Db 2524 GTCTGAGACTCCACCGTCCCGCTGTGAAGCTCATGTGTGAGACATCTACAGCGCTCC 2583
Qy 519 SerGlyThrIleLeuSerProGlyIleTrpProGlyPheTrpValAspAlaLeuSerCysAla 538
Db 2584 AGCGAGTCATTTTGGCTCTGAGATGGCCAGAGATATATATAGATTTCTTTACATTGTGAA 2643
Qy 539 TrpValIleGluAlaGlnProGlyIleTrpProIleTrpPheAspArgPheLeuThr 558
Db 2644 TGGATTAATGTAAGCAAAACAGGCACTCTTCAAAATGACTTTTGAAGATTTCAAGACA 2703
Qy 559 GluValAsnTrpAspThrLeuGluValArgAspGlyArgThrTrpSerAlaProLeuIle 578
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Db 2764 GGCAGATGCCAGGACCCAGGCAACCCAGATTTCTCATCAGACCCGGGAACTTCATGTAC 2823
Qy 599 LeuLeuPheSerThrTrpAspTrpSerHisSerAspIleGlyPheGlnLeuArgTrpGluThr 618
Db 2824 CTGCTGTTTCAACCTGACCAACAGCCGCTCCAGATCGGCTTCCATCCATCACTAGAGCT 2883
Qy 619 IleThrLeuGlnSerAspHisCysLeuAspProGlyIleProValAsnGlyIleArgHis 638
Db 2884 GTGACGCTTGAAGTGAGATTCCTGCTGAGCCCGGCAATCCCTGTGAACCGCCATTCGCCAC 2943
Qy 639 GlyAsnAspPheTrpValGlyAlaLeuValThrPheSerCysAspSerGlyTrpThrLeu 658
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Qy 659 SerArgGlyLeuProLeuGlnCysGluProAspPheGlnTrpSerArgAlaLeuProSer 678
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Qy 679 CysGluAlaLeuCysGlyGlyPheIleGlnGlySerSerGlyThrIleLeuSerProGly 698
Db 3064 TGGACGCTCTATGTGAGGCTACATCAAGGAGAGGAAAGGTGAACAGTCTTCTCTGGG 3123
Qy 699 PheProAspPheTrpProAsnAsnLeuAsnCysThrTrpIleIleGluThrSerHisGly 718
Db 3124 TTTCAGATTTTATCAAACTCTTAACCTGACAGGTGAACCTTAAAGTCTCATGGG 3183
Qy 719 LysGlyValPhePheThrPheHisThrPheHisLeuGlnSerGlyHisAspTrpLeuLeu 738
Db 3184 AAGGAGTTCAAAATGATCTTTACACCTTTCATCTTGAGAGTTCCACACATATTATACG 3243
Qy 739 IleThrGluAsnGlySerPheThrGlnProLeuArgGlnLeuThrGlySerArgLeuPro 758
Db 3244 ATCAACAGAGATGGAAGTTTTCAGAGCCCGTTGCCAGGCTCACCGGGGTGGTGGCT 3303
Qy 759 AlaProIleSerAlaGlyLeuTrpGlyAspPheThrAlaGlnValArgPheIleSerAsp 778
Db 3304 CATACAGAGATGGAAGCTTGTGGAACTTCACTGAGCCAGCTTGGTTTATATCAGAC 3363
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Qy 799 GluGluProGluValProAlaTrpSerIleArgGlyLeuGlnPheGlyValGlyAsp 818

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Db 3424 GATGATCTCGAGATCTCCCTGCTTACGCCAGAAAGATTTGTTTCACTTGTGTGGAGAC 3483
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Db 3484 TCTCTAGAGTTTCTCGTCTTCCGGGATATCGTTTGAAGGTGCCCAAGACTTACTTCC 3543
Qy 839 LeuGlyValArgArgLeuTrpSerSerProLeuProArgCysValAlaGluCysGly 858
Db 3544 CTGGGTGGGGCGCCGCTGTGTGAGATGACACTTCCCAAGGTGTGTGGCCGAATGTGA 3603
Qy 859 AsnSerValThrGlyThrGlnIleLeuLeuSerProAspPheProValAsnTrpAsn 878
Db 3604 GCAGTGTCAAGAAATAGAAATAGAAATATTAAGTCTTCCAAATTTTCCATCCAAATATGAT 3663
Qy 879 AsnAsnHisGluCysIleTrpSerIleGlnThrGlnProGlyLysGlyIleGlnLeuLys 898
Db 3664 AATACCATGAGTGATCTATAAATAGAAACAGAACCGGCAAGGCACTCACCTTAGA 3723
Qy 899 AlaArgAlaPheGluLeuSerGluGlyAspValLeuLysValTrpAspGlyAsnAsn 918
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Db 3784 TCTCACTGCCACTGGGCACTGCTCACTAAATAGAACTTCTGGGCTGATCTTAAGAC 3843
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Db 3844 ACATCCAAATCACTTATGCTGATGATTCACCAACCAATGATTCGACACCAAGGATTTT 3903
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Qy 1019 TrpAspArgProLeuProThrCysValAlaGluCysGlyGlyThrValArgGlyGluVal 1038
Db 4084 TGGGCAAAACCACTACCTCTGTCATGACGGAATGTGTGATCATGATCATGACGCCACA 4143
Qy 1039 SerGlyGlnValLeuSerProGlyTrpProAlaProTrpGlyLysHisAsnLeuAsnCysIle 1058
Db 4144 TCAGGACGAATATGTGCTCCCTGGCTATTCAGACTCCGATGACAAACCTCCACTGCAC 4203
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Db 4264 GAGATGGCTCAACATCTCTAAGAGTGTGGACCGGCGGTGACATGACATCTCTG 4323
Qy 1099 LysGluLeuSerGlyProAlaLeuProLysAspLeuHisSerThrPheAsnSerValVal 1118
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Qy 1119 LeuGlnPheSerThrAspPhePheThrSerTrpGlnGlnIlePheAlaIleGlnPheSerVal 1138
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Qy 1139 SerThrAlaThrSerCysAsnAspProGlyIleProGlnAsnGlySerArgSerGlyAsp 1158
Db 4444 TCATTTGACGACCTGTAAAGATCCAGATATGCCCAAAATGGACCCGCTATGAGAC 4503
Qy 1159 SerTrpGluAlaGlyAspSerThrValPheGlnCysAspProGlyTrpAlaLeuGlnGly 1178

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Db 4504 AGCAGAGAGGCTGGAGACACCGTCACATTCAGTGTGACCTGGCTATACGCTCCAGAGA 4563
Qy 1179 SerIaGluIleSerCyValValIleGluAsnArgPheProGlnProSerProPro 1198
Db 4564 CAAGCCAAATATCAGCTGTGACGACTGAATTAACGGGTCCTTTGGCAACAGACCTCTCT 4623
Qy 1199 ThrCysIleAlaProCysGlyGlyAspLeuThrGlyProSerGlyValIleLeuSerPro 1218
Db 4624 ACATGCACTAGCTGCTTGTGAGGGAATCTGACGGGCCACGAGGTGTTATTTTGTCCACC 4683
Qy 1219 AsnTyProGluProTyProProGlyValGlyGlyCysAspTyrValIleValIleSerPro 1238
Db 4684 AACTACCCAGACCGCGTATCTCTCGGAGGAATGTACTGAGAGTAAAGTAAAGTAAACCGG 4743
Qy 1239 AspTyrValIleAlaLeuValPheAsnIlePheAsnLeuGluProGlyTyrAspPheLeu 1258
Db 4744 GACTTGTCACTCCGCTTGATATTCAAAAGTTTCAACATGGAGCCACACTATGACTTCTTA 4803
Qy 1259 HisIleTyrAspGlyTyrAspSerLeuSerProLeuIleGlySerPheTyrGlySerGln 1278
Db 4804 CACATCTATGAGGGAGAGATTTCCACAGCCCTCTATGGAGATTACAGGGCTCTCAG 4863
Qy 1279 LeuProGlyValIleGlyLeuSerSerAsnSerLeuPheLeuAlaPheArgSerAspAla 1298
Db 4864 GCCCAGAAAGATAGAGAGTACGGGAACAGCTGTTCTGGCATTTCGGAGTATGCC 4923
Qy 1299 SerValSerAsnAlaGlyPheValIleAspTyrThrGluAsnProAlaGlyLeuSerPhe 1318
Db 4924 TCCGTGGCCCTTTCAGGGTTCGCCATTTGAATTTAAAGAAACACCGGAAGCTGTGTTT 4983
Qy 1319 AspProGlySerIleValAsnGlyThrArgValIleSerAspLeuValLeuGlySerSer 1338
Db 4984 GACCCAGAAATATATGATGATGAGCAAGAGTTGGACAGACTTCAAGCTTGCTGCACAC 5043
Qy 1339 ValThrTyrTyrCysHisGlyGlyTyrGluValGluGlyThrSerThrLeuSerCysIle 1358
Db 5044 ATCACTACACAGTGTGACTGCTGCTATGAATCTTGACCCCTCATCATCAGCTGTGTG 5103
Qy 1359 LeuGlyProAspGlyValProValITPAsnAsnProArgProValCysThrAlaProCys 1378
Db 5104 ATTGGGGCTGATGGAAACCTCTCGGAGCCAGAGTGTGCTCTCCATATGCTCCCTGT 5163
Qy 1379 GlyGlyGlnTyrValGlySerAspGlyValValLeuSerProAsnTyrProGlnAsnTyr 1398
Db 5164 GAGAGCCAGTACAGGGAATCAAGAGGGTACTTTATACCAACATACCCCATATATAC 5223
Qy 1399 ThrSerGlyGlnIleCysLeuTyrPheValThrValProValAspTyrValIlePheGly 1418
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Db 5404 GCTACGTCAATCAATATTCGCTCGCATTCAGTCCAAAGAGCGGTGCTGCCGGGGC 5463
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Db 5704 TTCACTCAACGAAGAGTACATCTGTCCCGGGGATCCCTGAGGCATACGGAACAC 5763
Qy 1579 LeuAsnCyValITryValIleValProGluGlyAlaGlyIleGlnIleGlnValIle 1598
Db 5764 TTGAACGTATATGAAATCATATGATTCAGAGGGCTCGGAATTCAGATTCAGAGAT 5823
Qy 1598 IserPheValThrGluGlnAsnTyrAspSerLeuGluValPheAspGlyAlaAspAsn 1617
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Qy 1638 SerAsnGlnLeuTyrIleuHisPheTyrSerAspIleSerValSerAlaAlaGlyPheHis 1657
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DB 7684 ATGGTGGGCGACAGCAATGCACTGTAGACAAACCCACTTGGCATGACAGTGGAC 7743
QY 2238 GluAlaIleProLeuCysGlnAlaLeuSerCysGlyLeuProGlnAlaProLysAsnGly 2257
DB 7744 TCCCTACGCACTCTGCGAGGCTGTGCTGTGAGATCCAGAAATCCCGAGAAACCGT 7803
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Qy	2738	SerasnalaargvalvalpheserabrglyleuvalpheserSerlevaltyrcslu	2757
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Qy	2818	ProglyltyrmetetgluserhiarargvalserValleuserCysthrlyasabrgthr	2837
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Oy		3018	GlyThrProAdeCyValProHisieCysArgInProGluIurnProThrHisAla	3037
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Oy		3038	AsnValGlValAleuAspLeuProSerMetCylTyrrHrleuile-ThrProAlaAarg	3057
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Oy		3057	gAlaSerProserArgValAlaProserThrAlaProAlaArgmetAlaIagIyl	3077
Dd		9673	GGCTTTTCTCCGAGGGGATCTGACACAGAACAATGTAAAGACACATAATGACA	9732
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Dd		9733	GGAAAGTCGC	9742
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DEFINITION		Homo sapiens CUB and sushi multiple domains 3 (CSMD3) mRNA,		
ACCESSION		AY210419		
VERSION		AY210419.1		
KEYWORDS		GI:30908444		
SOURCE		Homo sapiens (human)		
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
REFERENCE		Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
AUTHORS		Lau,W.L. and Scholnick,S.B.		
JOURNAL		Identification of two new members of the CSMD gene family		
AUTHORS		Genomics 82 (3), 412-415 (2003)		
TITLE		2 (bases 1 to 12486)		
JOURNAL		Lau,W.L. and Scholnick,S.B.		
FEATURES		Direct Submission		
source		Submitted (02-JUN-2003) Ocularryngology - Head & Neck Surgery, Washington University School of Medicine, 660 South Euclid Ave., Saint Louis, MO 63110, USA Location/Qualifiers 1..12486 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" 1..12486 /gene="CSMD3" 142..10647 /gene="CSMD3" /note="contains 14 CUB domains and 27 sushi domains" /codon_start=1 /product="CUB and sushi multiple domains 3" /protein_id="AA034702.1" /translation="MGIKSGPTFWNIWFLITVSCVKPFICTCGTLKINGINTISPGF PYGPNGANCTWVIABERNRIQIVPOSFALIEEYDILSYLDGHPRHTNRTLRTPR LPBPVTSTKSVSLRLTSDFAVSAHGKRYVEELQSSCCAGVPYPKGVLIGTFVDVG DKIRYSCVTGLIDGHPLQICIANSVNTASNDPEVPICRADAGCGTMRGSGIIISBE SPISPHNNADCTTIVAEPDDTSLFTDFOMEKEKYDLIEEGSEPTLWLSGNMIFLE PILSNOMWLRFHVTDNSNRHGFSAIPYOVKRIDFSRGFKLFGKDNKNKSI LNKY EGCIKTASNCPDDEPENGKRIGSDPSLGSTVGLSCDEVVLQGAKSITCORIAEVFA AAMDHPVCVKTKCSNLQSPSTPIPSNPFPDYDSNAOCWWITATVNKKIOINPMR AEFLELIGDTLLTIGDGGEVDPRTVLQVLFGSVPLIVMSQMWHLQDTDSVGS VGFVANPKIEKESCGDPGRPLVGRIGDSESNDVRFEQGFSELIGEKSYLCQEN NOMGANPICIFCLSNFFAAPMTGVSLPDVEEGNNLNCWTIISDPGSHISFNPD FDLESODPLAFVAGDSESPILCTFGAEGVSHLTNSHSLRLKEPADMSRGFNRL ITYTNFHNEGPCDGIPIINARFGDNDOSSISLVIEBEGIKTQGNETLICIMDGK VMMSGILPKCGAPCGHFSAHSVLIISPMPGYKSDINCMEVTEARGHSIKITPERP FORLANTLVSEHDGPNLSPSLGISTGVDPQPLRESSNFYLLFTTDSRNNGKFR IHVESVNTNVSCIDPGLPVHGRERYGDFSIGSTVSFCOSGNYLSHEEPLCKNMHM		

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ORIGIN

Alignment Scores:

Pred. No.: 0 Length: 12486
 Score: 10384.00 Matches: 1798
 Percent Similarity: 74.62% Conservative: 492
 Best Local Similarity: 58.59% Mismatches: 659
 Query Match: 61.14% Indels: 120
 DB: 9 Gaps: 10

US-10-016-248-2 (1-3104) x AY120419 (1-12486)

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 QY 18 Asp-----CyCyAlSerAenGlnArgHisSerValGly 29
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 DB 1042 TTTAGGCTCCCATATGAATGAAAAAGCCATAGATTTTAAATCTAGAGGATTTAAATTG 1101
 QY 50 MetProSerIyAeApsAnsSerGlnIyGlnHrSerValLeuThrGlnValGlyValSerGln 69
 DB 1102 TTTCCAGGGAAGACAAACAGCAAGTTTCTATCTTAATAGAGAGGATTTAAACA 1161

QY 70 GYHISAMetCySPROASpProGlyIleProGlyuArgGlyIyYsArgLeuGlySerAap 89
 DB 1162 GCTTCAATTATATGCCCAATCCAGAGAACGAAAGGAAAGGAAATCCGATCATGAT 1221
 QY 90 PheArgLeuGlyIySerValGlnPheThrCyAenGluGlyTyraSpleuGlnIySer 109
 DB 1222 TTTAGCCTTGGACCACTGACGCTCTTGTGATGAAGATTAATCTCTACAGGGCGCA 1281
 QY 110 LysArgIlethCyMetIySValSerApmMetPheAlaIleThrSerSphIsaGPro 129
 DB 1282 AATAGCATACCTGTCAAGGATAGCTGAAGTTTCTGCTTGAGATACACAGCCT 1341
 QY 130 ValCyArgAlaArgMetCyAspAlaHisLeuArgIyProSerGlyIleIleThrSer 149
 DB 1342 GTGTGTAAGTGAAACGTTGCTCTTAATCTTCAAGGACCAAGTGATCTTACATCT 1401
 QY 150 ProAenPheProIleGlnIyAeApsAnsAlaHisCySValITripIleIleThrAlaLeu 169
 DB 1402 CCCACCTTCCGTTCCAGATATACGCAATGACAAATGTGTGGGTATCTACACAGCTG 1461
 QY 170 AenProSerIyValIleIyLeuAlaPheGluGluPheApsLeuGlyuArgGlyTyraS 189
 DB 1462 AATACAAATTAAGTTATCCAGATTAATTTGAAAGAAATTTGATCTGAGATTCGCTATGAT 1521
 QY 190 ThrLeuThrValGlyAspGlyGlnAspGlyAspGlnIyLeuThrValLeuTyrrwSer 209
 DB 1522 ACCCTTGACAAATGGAGATGGGGCCAAATGGAGATCTTACAGACAGTCTCCAAAGTG--- 1578
 QY 210 GlnAmaAlaCySerApsSerProIleThrProGlySerArgIleProGlu----- 226
 DB 1579 -----CTGACTGACACCTTTGACGACACTTGAATG 1611
 QY 227 SerMetSerGlyAspIleITripArgGlnIySerITripValLeuGlnIleCyArgSple 246
 DB 1612 AAGCATAGATGACCAATATGCTGACCTCAAGC----- 1647
 QY 247 SerSerSerAapAlaArgSerGlySerValArgIySerProIySphSerAmaAlaVal 266
 DB 1648 -----GACGAAAGTGTGGATCTGTGTTCAAGTTAACTACMAA----- 1689
 QY 267 GlnLeuValAlaProGlyIThrGlnIleGluGlnIySerCySValAspProGlyIlePro 286
 DB 1690 -----GAAATGAGAAAGAAAGTTGTGATCTCTGATACACC 1728
 QY 287 AlaITyrgIyAgaGluGluGlySerArgPheHisIleGlyAePThrLeuLysPheGluCyS 306
 DB 1729 TTAATGGAATTAAGAGAGCGATGATTTTCTATGCTGATGTTTAAAGTTTGAATGC 1788
 QY 307 GlnProAlaPheGluLeuValGlyGlnIyAlaIleThrCySglnIySaaAenGlnITrip 326
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 QY 327 SerAlaIySlySPProGlyCySValPheSerCyAePheApsPheThrSerProSerGly 346
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 QY 427 PheGlnIThrApsHisSerIThrGlyIySArgGlyPheApmIleThrPheThrIThrPheArg 446

Db 2149 TTTACGGCTGACCACTCAATGTCAGAGCGTGGCTTTAACTTCACTTCAACACTTTTGA 2208
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Db 2209 CATATGAAATGCCCTGATCCCTGATCCATCAATCAATCAGCGCTTTGGGAGCAACTTT 2268
Qy 467 GlnLeuGlySerSerIleSerPheLeuCyAapSerIleGlyPheLeuGlyThrGlnGlySer 486
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Db 2329 GAATCATTTACATATATTTCTTATGATGAGAAATATATGAGAGTGAAGTCAATCCAAA 2388
Qy 507 CysGlnAaProCysGlyGlyValIleuThrSerProSerGlyThrIleLeuSerProGly 526
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Qy 527 ThrProGlyPheThrCysAapSerIleLeuSerCysValIleThrValIleGlnAaProGly 546
Db 2449 TGGCAGAGATACATCAAGAGCTTTTGAATTTGAGTGGGATTTGAAGCTGAACCTGGA 2508
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Qy 567 ValArgAapGlyArgThrTyrSerAaProLeuIleGlyValIleGlyValIleGlyVal 586
Db 2569 GTTCATATGAGGCGCAATCTTCTGTCACTTCCTGATGATCTTCAATGAGCAACCAAGTG 2628
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Qy 627 LeuAapProGlyIleProValaenGlyGlnAaRhiGlyAaenAapPheTyrValIleGlyVal 646
Db 2749 TTGGACCTGCGCATACCTGTACAGCGCTGCTATGATGATTCATGATTTCTCATTTGGGCTCT 2808
Qy 647 LeuValIlePheSerCysAapSerGlyTyrThrIleuSerAapGlyGlnProLeuGlnCys 666
Db 2809 ACTGTTTCATTTATTTGATTTGATTCAGATACAGGTTGAGTCAAGAAAGCCCTTCTATGC 2868
Qy 667 GlnProAapPheGlnIleTPSerArgAlaLeuProSerCysGlnAaIleuCysGlyIlePhe 686
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Db 2989 CTGAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3048
Qy 727 ThrPheIleLeuGlnSerGlyValIleAapTyrIleuLeuIleThrGlnAaenGlySerPheThr 746
Db 3049 ACTTTTATTTGAGAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3108
Qy 747 GlnProLeuAaRhiGlnLeuThrGlySerArgLeuProAaProIleSerAaIleGlyLeuTyr 766
Db 3109 CAACCACTGCGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3168
Qy 767 GlnAaenPheThrIleGlnValaRhiGlnPheIleSerAapPheSerMetSerTyrGlnGlyPhe 786
Db 3169 GGAATTTTCAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3228
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Qy 827 GlnTyrArgLeuGlnGlyThrIleAaRhiIleThrCysLeuGlyGlyArgAaRhiLeuTyr 846
Db 3349 GGTATGACTGAGAGAGACATCAAGATATATCTGTCTTGTGTGTGTGTGTGTGTGTGTGTGT 3408
Qy 847 SerSerProLeuProArgCysValaIleGlyCysGlyAaenSerValIleGlyThrGlnGly 866
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Qy 867 ThrLeuLeuSerProAaenPheProValaenTyraenTyraenAaenAaenAaenAaenAaen 886
Db 3469 ATTTGCTGCTCCAAATTTATCCATCACTCAATGAAACCAACATGATATCATTTATAGT 3528
Qy 887 IleGlnThrGlnProGlyIleGlyIleGlnLeuValaRhiAaRhiAaRhiAaRhiAaRhiAaRhi 906
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Qy 947 PheIleThrAaPheAaIleuAaenThrSerIleGlyPheGlnLeuIleHisPheSerPheGln 966
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Qy 967 LeuIleLeuCysGlnAapProGlyThrProValaPheGlyTyrIleValIleAaPheGly 986
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Qy 1087 IleThrAaPheProValaIleuSerGlyValLeuLeuGlyLeuLeuSerGlyProAlaLeu 1106
Db 4129 GTCTGGAGCGGTCCACAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4188
Qy 1107 ProValaPheLeuHisSerThrPheAaenSerValaIleuGlnPheSerThrAapPhePhe 1126
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Qy 1127 ThrSerIleGlnGlyPheAaIleGlnPheSerValSerThrIleThrAaenSerCysAaAaP 1146
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Db 4309 CAGGCGGTCCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4368


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Db 4369 GTTTTCATGTGATGACCAAGATATGAACTTCAGAGGAGGAAAGAAATACCTGGCATTCAG 4428
QY 1187 IleGluAsnArgPheMetIleProSerProGlyCysIleAlaProCysGly 1206
Db 4429 GTGAAATCGGTAATCTTGGAGCCGACCCACAGTGTGTATAGCACTCGTGGAGGC 4488
QY 1207 AspLeuThrGlyProSerGlyValIleLeuSerProAsnTyrProGluProTyrPro 1226
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QY 1227 GlyGluCysAspTyrPheValThrValSerProAspTyrValIleAlaLeuAlaPhe 1246
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QY 1247 AsnIlePheAsnLeuGluProGlyTyrAspPheLeuHisIleTyrAspGlyArgAspSer 1266
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QY 1267 LeuSerProLeuIleGlySerPheTyrGlySerGlnLeuProGlyArgIleGluSerSer 1286
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QY 1287 SerAsnSerLeuPheLeuAlaPheArgSerAspAlaSerValIleAsnAlaGlyPheVal 1306
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QY 1307 IleAspTyrThrGluAsnProArgGluSerCysPheAspProGlySerIleValAsnGly 1326
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QY 1327 ThrArgValGlySerAspLeuValLeuGlySerSerValThrTyrTyrCysHisGlyGly 1346
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Db 5149 CTCACAGATGTTGTGAGGTATGATGAGCCCACTCAGCAATCTTCTGTATATCTTCC 5208
QY 1447 LeuSerGlySerHisThrGlyGluSerLeuProLeuAlaThrSerAsnGlnValLeuIle 1466
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QY 1507 GlySerAspPheSerValGlyAlaIleValaLysPheGluCysAsnSerGlyTyrAlaLeu 1526
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QY 1547 SerAlaProThrCysValValProCysGlyGlyAsnLeuThrGluArgArgGlyThrIle 1566
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Db 6349 GGGTTTCATATGTATACCAAGCTTACGTTGCCAAGCTGCTTATATCAGCCCGCTTT 6408
QY 1847 AlaAsnGlyIleValArgGlyAlaGlyTyrAsnValGlyGlnSerValThrPheGluCys 1866
Db 6409 CGAAATGGTTTGTAAATGTATGATGATTTAGTGTGGTCAAAACATTCATTTGATGT 6468
QY 1867 LeuProGlyTyrGlnLeuThrGlnHisProValIleuThrCysGlnHisGlyThrAsnArg 1886
Db 6469 TTCCAGGATACCAATTAATGGAATTCAGCTCTCACATGCTTCCAGGATCTAGTCTGT 6528
QY 1887 AsnTyrAspHisPheProLeuProLysCysGluValProCysGlyGlyAsnIleThrSerSer 1906
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Db	6529	AATTGGATCATCCACTTCCAAAGGTGTAAGCTCTTTGTGGGAATATACCTGCATG	6588
Oy	1907	AaaglythValTySerProGlyPheProSerProTySerSerSerGlnAspCyVal	1926
Db	6589	AATGGACCACTATTATCTCCTGGGTACTGTGTAATATCCAAACTTTCAAGATTGTTT	6648
Oy	1297	TTPLeuLiethrValProIleGlyPHIleGlyValArgLeuAenLeuSerLeuLeuGlnThr	1946
Db	6649	TGGCTTTGTAAAGATACCCCTGGGAATGGCATCTACCAATTTTATCTGCTTCAACA	6708
Oy	1947	GIUProSerGlyAspPheIleThrLleThraapGlyProGlnGlnThrAlaProArgHeu	1966
Db	6709	GAACCAATATATGATTATTAATCTGATAGGATGGAGTGCACACCAAAATTCACCTCAGATC	6768
Oy	1967	GlyValPheThrArgSerMetAlaLeuValSerThrValGlnSerSerSerAsnGlnValLeu	1986
Db	6769	GGTCACTTCAGTGGCAATACCGCTTTGGAAATCAGTCTACAGTACTTCAATCAGATTCTA	6828
Oy	1987	LeuLybPheHlBarGAPAlaAlaThrGlyGlyIlePheAlaIleAlaPheSerAlaTy	2006
Db	6829	ATCAAAATTCACAGATGATTTCAACAAGTGGCTTTTGTGCTCAGATTACAGCCATAT	6888
Oy	2007	ProLeuThrLybCybProProProThrLleLeuProAsnAlaGluValValThrGlnAsn	2026
Db	6889	CAACTAAGGGTGTGCAACCTCCACACCTGTGCCAATGCTGAATTTTACCGAAGAT	6948
Oy	2027	GIUGluPheAsnIleGlyAspIleValArgTyArgCybLeuProGlyPheThrLeuVal	2046
Db	6949	GATGAATTTGAAATAGTGATATATTAATAGTATCAGTCTCTCCAGATTTACTTTAGT	7008
Oy	2047	GlybAngIuIleLeuThrCybLybLeuGlyThrTyLeuGlnPheGluGlyProProRo	2066
Db	7009	GGTATATCAATTCCTGACCTGCAGATTAGAGAACACGATCGAGATGAGACACTCCA	7068
Oy	2067	IleCybGluValHlHleCybProThraPheAsnIleuLeuThrAapSerThrGlyValIleLeu	2086
Db	7069	GTTTGTCNAGGCTCTGTCTGCTGCCAATAATTAACGGCTAGATTTCTACGTGAGTCATATGG	7128
Oy	2087	SerGlnSerTyProGlySerTyProGlnPheGlnThrCybSerThrLeuValArgAl	2106
Db	7129	AGCCTGGATATCTCGACAGTTATCCCAATCTTCAAAATGTGTGATGATGAGCATTTCACT	7188
Oy	2107	GluProAspTyTyAsnIleSerLeuThrValGluTyPheLeuSerGlyLybGlnTyAsp	2126
Db	7189	GAAGAAAGGTATTAATATCACCATGTTTGTAGATTTCTTCACAGACGAAAAAGAAATTCAT	7248
Oy	2127	GluPheGluIlePheAspGlyProSerGlyGlnSerProLeuLeuLybAlaLeuSerGly	2146
Db	7249	GTTCTTCAGGTATGATGAGCAAAATTTCAAAATCCAGTGTATTTCTCTCAGTGGG	7308
Oy	2147	AsnTySerAlaProLeuIleValThrSerSerSerSerAsnSerValTyLeuArgTyrSer	2166
Db	7309	GATTAATTAATCTGCTTTAATATTAACAAAGCAATGTCTATGAAGTATTTCTTCAGTGGTCA	7368
Oy	2167	SerAPheHlAlaTyTyAsnArgLybGlyPheLybIleArgTySerAlaProTyCybSer	2186
Db	7369	CGAGATCATGCGAATTAACAAAAAGGCTTCGGAATACATATATATGCTTCTCACTGATGT	7428
Oy	2187	LeuProAlaGluAlaProLeuHlGlyPheIleLeuGlyGlnThrSerThrGlnProGlyGly	2206
Db	7429	ACACCAAGATCCCCCACTCAGATGATATTTATCACTCGACACAGGTGGCAGACTTAACAGT	7488
Oy	2207	SerIleHlAspPheGlyCybAsnAlaGlyTyArgLeuValGlyHlHleSerMetAlaIleCy	2226
Db	7489	GTGTGCTCGCTGGGCTGTGATCTGAGAGATTTCCGACTTTTGGAAAAAGCAGTGTGTGTC	7548
Oy	2227	ThraGhlAProGlnGlyTyThrIleuThrPserGluAlaIleProLeuCybGlnAlaLeu	2246
Db	7549	AGAAAGTCTCTCTATGGGATCATGATGAGGATGGCCAGTCCGTGCTGCAAGCAATT	7608
Oy	2247	SerCybGlyLeuProGluAlaProLybAngIyMetValPheGlyLybGluTyThrVal	2266

[illegible]

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 DB 8542 TCTGGGAGAAAGTATATCTTTGGGCTCTACTGCTTCTCTGACAGAAAGGCTCC 8601
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 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 MEDLINE
 PUBMED
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 2 (bases 1 to 10774)
 Chara, O., Nagase, T. and Kikuno, R.
 Direct Submission
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 292-0812, Japan (E-mail: cdnainfo@kazusa.or.jp,
 URL: http://www.kazusa.or.jp/huge, Tel: 81-438-52-3913,
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RESULT 14

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 VERSION AX537467.1 GI:25269270
 KEYWORDS
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

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 Hefalla, A.J., Ghandi, A.R., Thangavelu, K., Sanjanvala, M.M.,
 Tang, Y.T., Ramkumar, J., Griffin, J.A., Swarnaker, A., Azimzal, Y.,
 Sapperstein, S.K., Burford, N., Lee, E.A., Lu, Y., Tran, U.K. and
 Marquis, J.P.
 Molecules for disease detection and treatment
 Patent: WO 020709-A 38 12-SEP-2002;
 Incyte Genomics, Inc. (US)
 Location/Qualifiers

FEATURES

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 /db_xref="taxon:9606"
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ORIGIN

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 Score: 9077.50 Matches: 1720
 Percent Similarity: 86.47% Conservative: 5
 Best Local Similarity: 86.22% Mismatches: 8
 Query Match: 53.44% Indels: 265
 DB: 6 Gaps: 8

US-10-016-248-2 (1-3104) x AX537467 (1-6004)

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Db	1262	GAATAACAACACGAAATCATTTAAAGCCTTCAGGTCGACAGAGAAAAGCATCAATATT	1321
Oy	898	LysAlaArgAlaPheGluLeuSerGluGlyAspValLeuIleuValTyrAspGlyAsnAsn	917
Db	1322	TCACCCGAGAACGTTTCATTAAAGCTCAAGGGGAGTCTTCTTAAGATTATGTATGAAAAAT	1381
Oy	918	AsnSerIleAlaGlyLeuGluIleValPheSerHisSerGlnIleuMetGlyValThrLeuAsn	937
Db	1382	AAAACAACGACCTTAACGGGGCTTTCAACGGGTGCGCTATGCGAGACGTGACCTAAGC	1441
Oy	938	SerThrSerSerSerLeuTyrIleuAspPheIleThrAspAlaGluAsnThrSerLeuGly	957
Db	1442	AGCAATCAATATCAAGCTCTGGCTAGATTAAATTTCACTCTGAAGGACAGATGAAGGC	1501
Oy	958	PheGluLeuHisPheSerSerPheGluLeuIleLysCysGluAspProGlyIleTyrProLys	977
Db	1502	TTTCAACTGTCCTCAACCAAGTTTGAATCTTTCATTGTGAAGCCACGAGCATTTCCAGC	1561
Oy	978	PheGlyIleTyrLysValHisAspGluGlyHisPheAlaGlySerSerValSerPheSerCys	997
Db	1562	TTTGGATTATAGATCAAGTCAACGAGTCACTTGGCTGGACAGACATCATCTATGATGC	1621
Oy	998	AspProGlyIleYSerSerLeuArgIleSerGluIleuLeuLeuCysIleSerGlyIleuArg	1017
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Oy	1018	ThrTyrAspArgProLeuProThrCysValAlaGluCysGlyIleTyrValArgGlyIleu	1037
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Oy	1038	ValSerIleGlnValLeuSerProGlyIleTyrProAlaProTyrGlnHisAsnLeuAsnCys	1057
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Oy	1058	IleTyrThrIleGluAlaGluAlaGlyCysThrIleGlyLeuHisPheLeuValPheAsp	1077
Db	1802	ATGTGATGATCGAAGTATGCCAGGAAACATTTGAAGCTTCAAGTTCTTCTGCTTGCAT	1861
Oy	1078	ThrGluIleuValHisAspValLeuArgIleTyrAspGlyTyrValGluSerGlyValLeu	1097
Db	1862	ACAGAAAGCCACATGATATATCTCGAGTTTGGGATGGTCCACAGAAAACGAGATGCTA	1921
Oy	1098	LeuLysGluLeuSerGlyTyrProAlaLeuProLysAspLeuHisSerThrPheAsnSerVal	1117
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Oy	1118	ValLeuGlnPheSerThrAspPhePheThrSerIleGlnGlyPheAlaIleGlnPheSer	1137
Db	1982	ACTATCCAAATTTGATACGAACTTTATATACGACAAATCTGATTCGCAATTCAGTTTCA	2041
Oy	1138	ValSerThrAlaThrSerCysAsnAspProGlyIleProGlnAsnGlySerArgSerGly	1157
Db	2042	AGTTCAATTCGAATGCTGCTGTCGATCCAGAGAGTCCCATGATGGACACGGAATGAT	2101
Oy	1158	AspSerTyrGluAlaGlyAspSerThrValPheGlnCysAspProGlyIleTyrAlaLeuGln	1177
Db	2102	GACGACGAGAAACCTGGGGACACAGTGTCTTTTCAGTGCATCTCGGATATGAGCTTCAA	2161
Oy	1178	GlySerAlaGluIleSerCysValLysIleGlnAsnArgPheThrPsnInProSerPro	1197
Db	2162	GGACAGAAAGAAATACCTGATATCCAGTGAAGAAATGATATCTTGGCAGCCGACGCCCA	2221
Oy	1198	ProThrCysIleAlaProCysGlyIleAspLeuThrGlyProSerGlyValIleLeuSer	1217
Db	2222	CCAGTCTGTATAGCACTTGATGGAGGCAATTTAACAAGATCTTCAAGCTTATTCCTTTCG	2281
Oy	1218	ProAsnTyrProGluProIleTyrProProGlyLysGluCysAspTyrIleValThrValSer	1237


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Qy      1258 LeuHisIleTyrAspGlyArgAspSerLeuSerProLeuIleGlySerPheTyrGlySer 1277
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Qy      1278 GlnLeuProGlyArgIleGluSerSerSerAsnSerLeuPheLeuAlaPheArgSerAsp 1297
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Qy      1298 AlaSerValSerAsnAlaGlyPheValIleAspTyrThrGluAsnProArgGluSerCys 1317
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Qy      1318 PheAspProGlySerIleLysAsnGlyThrArgValGlySerAspLeuLysLeuGlySer 1337
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Qy      1338 SerValThrTyrTyrCysHisGlyGlyTyrGluValGluGlyThrSerThrLeuSerCys 1357
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Qy      1358 IleLeuGlyProAspGlyLysProValTyrAsnAsnProArgProValCysThrAlaPro 1377
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Qy      1718 TyrProProPheLeuCysIleAlaGlnCysGlyGlyThrValGluGluMetGluGlyVal 1737
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Qy      1818 HisSerAspHisSerGlnAsnArgProGlyPheLysLeuGlnTyrGlnAlaTyrGluLeu 1837
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Qy      1918 ProTyrSerSerSerGlnAspCysValTyrPheIleThrValProIleGlyHisGlyVal 1937
Db      4172 GAATATCCAAACTTCCAAAGCTCTTTGGCTGTGAAGTTCCTCCCTGGAGATGGAGATC 4231
Qy      1938 ArgLeuAsnLeuSerLeuGlnThrGluProSerGlyAspPheIleThrIleTyrPhe 1957
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Db	4352	GTAATACAGACTTCCAAATTCMAATTTTATATCAAAATTCACAGTACTTCAACAAGTGGC	4411
QY	1998	ILEPHEALALEVALPHESESERALATYRPROLEUTHRYSCYSPROPROTHRIILEUEN	2017
Db	4412	TTTTTTGGTCAGTTATCATGCTTACCAACTGAGAGTGTGCAACCTCCACCACTGTCTC	4471
QY	2018	PROHEMALIAGLYVALVATHRGUASNGULGUPHEANLIEGLYAPRIIEVALARGTYR	2037
Db	4472	CCTAATGAGAAATCTCTACAGAAAGATATGATGATTGAANAAGCGAATTTATACAGATAT	4531
QY	2038	ARGCYBLEUPROGLYPHEPHEPHEULEVALGLYASNGULIELEUTHRCYVSEULEUGLYTHR	2057
Db	4532	CAGTGTCTTCAGAGGTTTACACTGTGTTGGCAATGCMAATTCGACATGCAGATTTGGAGAG	4591
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Db	4712	CAGATGTGTGGTGGAGCATCTCAAGTGGAAAGGTTATTAACATCAGCATGTGTGTGAA	4771
QY	2118	TYRPHLEUSERGLYUGLYGINTYRASPGLUPHEGLULIPEHASPGLYPROSEGLYGLN	2137
Db	4772	TTCTTCCACAGACAAAGAGTGTGATGTCTTCCAGGTGATGATGACCAAAATTTACG	4831
QY	2138	SERPROLEULEULYBALALEUSERGLYASNTYRSEERAPROLEULIEVALITHSESER	2157
Db	4832	AGTCCAGGCTTAATTTCTCTCAGTGGAGATTATTCAGTCTGTTTAATGTAACAAGCAAT	4891
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Qy	2398	IlePheSerCyAsnSerGlyTyrTyrThrLeuValGlySerArgValaArgGluCyMetAla	2417
Dd	5612	ATCTTCACATGTGATTTGGAGATTCAATGCTTGTGGGCTCTGTGTGACGGAAATGCTCTCT	5671
Qy	2418	AsnGlyLeuTyrPsrSerGlySerGluValaArgCySerLeuIleGlyIleCyGlyTyrProGlu	2437
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Job time : 28524 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 18, 2004, 10:24:56 ; Search time 95 Seconds

(without alignments)
10564.019 Million cell updates/sec

Title: US-10-016-248-2

Perfect score: 16985
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1360919 seqs, 32331874 residues

Total number of hits satisfying chosen parameters: 1360919

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	14142.5	83.3	2669	15	US-10-016-248-4
3	11305	66.6	3564	15	US-10-016-248-45
4	10975	64.6	3508	15	US-10-016-248-46
5	10475.5	61.7	3389	15	US-10-016-248-47
6	10475.5	61.7	3389	15	US-10-016-248-47
7	9025.5	53.1	1958	15	US-10-016-248-47
8	7662.5	45.1	2352	14	US-10-016-248-47
9	7662.5	45.0	2306	14	US-10-016-248-47
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14	4226	24.9	1048	15	US-10-016-248-49

15	4209	24.8	1043	15	US-10-016-248-48	Sequence 48, App1
16	4143	24.4	1274	15	US-10-016-248-48	Sequence 11, App1
17	3174	18.7	613	9	US-09-799-514-9	Sequence 9, App1
18	2639	15.5	529	16	US-10-398-037-2	Sequence 2, App1
19	2555.5	15.0	839	16	US-10-398-037-2	Sequence 11, App1
20	1864.5	11.0	3567	14	US-10-028-248A-47	Sequence 47, App1
21	1864.5	11.0	3567	15	US-10-028-248A-47	Sequence 47, App1
22	1850.5	10.9	3594	9	US-09-911-842-4	Sequence 4, App1
23	1850.5	10.9	3594	13	US-10-150-821-4	Sequence 4, App1
24	1794	10.6	3571	9	US-09-911-842-5	Sequence 2, App1
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26	1793	10.6	3570	14	US-10-028-248A-6	Sequence 6, App1
27	1793	10.6	3570	15	US-10-028-248A-6	Sequence 6, App1
28	1790	10.5	3571	16	US-10-603-283-2	Sequence 2, App1
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33	1629	9.6	326	15	US-10-451-010-10	Sequence 10, App1
34	1555	9.2	2489	9	US-09-911-842-5	Sequence 5, App1
35	1555	9.2	2489	13	US-10-150-821-5	Sequence 5, App1
36	1470.5	8.7	3623	16	US-10-741-601-335	Sequence 335, App
37	1419.5	8.4	2050	9	US-09-898-570-22	Sequence 22, App1
38	1419.5	8.4	2050	10	US-09-898-570-22	Sequence 22, App1
39	1370	8.1	1251	15	US-10-311-623-12	Sequence 12, App1
40	1362	8.0	2044	15	US-10-276-774-2152	Sequence 2152, Ap
41	1353	8.0	1004	15	US-10-114-270-32	Sequence 32, App1
42	1350.5	8.0	2887	17	US-10-479-875-8	Sequence 8, App1
43	1306	7.7	505	15	US-10-108-260A-3257	Sequence 3257, Ap
44	1281.5	7.5	351	15	US-10-416-314-1	Sequence 1, App1
45	1266.5	7.5	1139	9	US-09-764-893-102	Sequence 102, App

ALIGNMENTS

RESULT 1
US-10-016-248-2
Sequence 2, Application US/10016248
Publication No. US20040033491AI
GENERAL INFORMATION:
APPLICANT: Alsebrook et al.
TITLE OF INVENTION: Protein and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-218
CURRENT APPLICATION NUMBER: US/10/016,248
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/254,329
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/291,037
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 60/255,648
PRIOR FILING DATE: 2000-12-14
PRIOR APPLICATION NUMBER: 60/297,173
PRIOR FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: 60/309,258
PRIOR FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: 60/326,393
PRIOR FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: 60/315,639
NUMBER OF SEQ ID NOS: 167
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
TYPE: PRT
ORGANISM: Homo sapiens
US-10-016-248-2
Query Match 100.0%; Score 16985; DB 15; Length 3104;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1861 SVTFECUPGYQLTGHVPVLTQHGTRNRMWDHPLPKCEVPCGANTTSSNGTYVSPGSPYS 1920
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Qy 1921 SSODCWLITVPIGHGRLNLSLQTEPSGDFITIMPQOYAPRLGVFRSNAKKTVOS 1980
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Qy 1981 SSNOVLLKFRHDAATGCIFAIAPSAYPLTKCPPTILPNAEVYTENDEFNIGDIVRYCL 2040
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3001 LLOSTTRTCLPNTLWSGTTPDCVPHHCROBETPTAHNVGALDLPMSGYTLITPARASP 3060
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PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/291,037
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 60/255,648
PRIOR FILING DATE: 2000-12-14
PRIOR APPLICATION NUMBER: 60/297,173
PRIOR FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: 60/309,258
PRIOR FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: 60/326,393
PRIOR FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: 60/315,639
PRIOR FILING DATE: 2001-08-29
NUMBER OF SEQ ID NOS: 167
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 2669.
TYPE: PRT
ORGANISM: Homo sapiens
US-10-016-248-4

Query Match 83.3%; Score 14142.5; DB 15; Length 2669;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 2605; Conservative 1; Mismatches 2; Indels 59; Gaps 3;

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Db 781 MSYEGFHTTSEIDLCEPEPEVPAVSIRKGLQFGVDTLTFCPEFGRLEGTARTICG 840
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Qy 1981 SSMQVILKTRDAATGCIPIALFASAVPLTKCEPPTLLPNAEVTENEENIGDIYRRLC 2040
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Qy 2430 ---AGHCGTPPIYNGHNGENBSYRGSVYVQCAGRLIGMSVRLICQDHMSGKTPFC 2486
Db 2430 LTKGHCHTPEPIYNGHNGENBSYRGSVYVQCAGRLIGMSVRLICQDHMSGKTPFC 2520
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RESULT 3
US-10-016-248-45
; Sequence 45, Application US/10016248
; Publication No. US20040033491A1
; GENERAL INFORMATION:
; APPLICANT: Alcobrook et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-218
; CURRENT APPLICATION NUMBER: US/10/016,248
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/254,329
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/291,037

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; PRIOR FILLING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/255,648
; PRIOR FILLING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 60/297,173
; PRIOR FILLING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: 60/309,258
; PRIOR FILLING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/326,393
; PRIOR FILLING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/315,639
; PRIOR FILLING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 45
; LENGTH: 3564
; TYPE: PR1
; ORGANISM: Mus musculus
; US-10-016-248-45

Query Match      66.6%; Score 11305; DB 15; Length 3564;
Best Local Similarity 63.8%; Pred. No. 0;
Matches 1960; Conservative 463; Mismatches 592; Indels 58; Gaps 8;

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      323  KMLPSKXSHKNSVLTGCVSLSDMCPDPGIPDNRRAGSDPFGVAGANVQFSCEDNYLQ 382
      108  GSKRITOMKYSDMFAASDHRPVRCARMCALHGRSGIITSPPFPIOVYNNACWVIT 167
      383  GAKGITQORVETETLAANNDRPICRATCGSNLKGPSGVITSPYVQYEDNACVAVIT 442
      168  ALNPSKVIKLAFFEEFDLERGYDILTVGDGQDQDKQTVLYMSQVACSDSPHTPSRIPE- 226
      443  TTPEDKVIKLAFFEEFELERGYDILTVGDAGKVDTRREVLY-----LIGSSVPLD 492
      227  --SMSGDIWROKMTVLEICRDISSDARSQSVKSPKTSNAVELVARG----TEIQGS 279
      493  IVSSNQMWLH-----LQSDDS-----IGSPFRAVYQELIKG 526
      280  CGDGIAYGRREGSRFHGDLTKFECOPAFELYGOKAITCQKNNOMSAKKPGVSCF 339
      527  CGDGIAYGKRTSSFLHGDTLTFECQAFELGSEVITTCQKNNOMSGKPPSCVSCF 586
      340  NFTSPSGVLSNPYPEDYGNHLICVWLILARPESRIHLAFNDIDVEPQDFLVIKQDATA 399
      587  NFTAPSGIILSPNPEYGNMNCVWLILISPEGRHILIFKDFPVEFCQDFLAVKDGIS 646
      400  EAPVLTGFSGNQLPSSITSSGVARLEFQTDHSTGKRGFNITFTTFRHNECPDPGVNG 459
      647  DITVLGTFSGNEVBAQALSSGHIIVRLTFQSDHSTTGGRFNITFTTFCQNECHDGIPIVNG 706
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      707  RRFEDRLLSSVSFHCDDGFKVQSSBSITCILQDANVWVSSVPPCEAPCGGHLTSS 766
      520  GTILSPMPGFKALSCAWIYEAQPGYIKITFDRKTEVNVYDTEVRODRYTSAPLIG 579
      767  GVILPMPGFKYKSLNCEWVIEAKPGHSIKITFDRKTEVNVYDTEVRODRYTSAPLIG 826
      580  VYHGTQVQPLISTSNLYLLFSTDKSHSDIGQLRYETITLQSDHCLDPGIPVNGRHG 639
      827  EYHGTQVQPLISTSNLYLLFSTDKSHSDIGQLRYETITLQSDHCLDPGIPVNGRHG 886
      640  NDFVGLVYTFSSCSGTYLSDGEPLCEPNFQWRALPSCCALCGGFTQSSGTTILSPG 699
      887  SNFIRSTLVTFSCDPTGLSDDEPLVCEKQNNHAPSCDALCGYIHGSGTVLSPG 946
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      1007  TTAGLFGNFTALRISDPSISYEGNTFAEYDLEPCDDPVAPASRIIGQFGVGD 1066
      820  LTFSCFPYRLESTAAITICGRRRLMSPLPFCVAECGNSVYGTCTLLSPNFVANN 879
      1067  LATTCQYRLBEATKLTICGRRRLMSALPFCVAECGNSVYGTCTLLSPNFVANN 1126
      880  NHECTYSIQTPGKGIQKARAFELSEBDVLYKYDGNNSARLLGVPSHEMVGTLNST 939
      1127  NHECTYSIQTPGKGIQKARAFELSEBDVLYKYDGNNSARLLGVPSHEMVGTLNST 1186
      940  SSSLMDFITDAENTSKGFEHLHSSFELKCEDPGPKPGYKXNDGHPAGSSVSRGCDP 999
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      1000  GYELRGSEELLCSGERRTWDRPLPFCVAECGTVGEVSGOYLSPGYPAPYEHNLNCIW 1059
      1247  GYAMHSSITLTCISGDRRWDRKMPSCVACGGLVHAATSGRLISGYPAPYEHNLNCIW 1306
      1060  TIEAAGCTTGLHFLVDETEVDVLRIMDPYSEGVLLKELSGPALPKDLSTPNSVLT 1119
      1307  TIEADPGKTIHLHFVDETEVDVLRIMDPYSEGVLLKELSGPALPKDLSTPNSVLT 1366
      1120  QESTDPTFSKQFALQFVSATASCNDPGLPONGSSSGSWEAGDSTVPCCDGYALQGS 1179
      1367  QFSDPFISSGFSIFSTSIASCTNDPMPQNGTRGDSREGGDTTTCDCDGYALQGS 1426
      1180  AELSCVKEIKRPFMOQSPPTCIPACGDLTGPSGVILSPYPPYPPGKCDMKVTPSPD 1239
      1427  AKITCQVQNNRPFMOQSPPTCIPACGDLTGPSGVILSPYPPYPPGKCDMKVTPSPD 1486
      1240  VYIALVENIENLEPGYDLHAYDGRDLSPLIGSFYGSQOLPGRIESSNSLFLAFRSDAS 1299
      1487  FVIALIFKSPMSPEYDFLHAYEGEDSNPSLIGSFYGSQOLPGRIESSNSLFLAFRSDAS 1546
      1300  VSNAGFYIDYTEMPPRESCTPFGSIKNGTRGSLKLGSSVTVYCHGYPEVGGSTLSCL 1359
      1547  VGLSGFAIEFKKPREKCFDPMGNIMGTRIGTFKLGSTVYTCDSGKVKIVDSSLECVT 1606
      1360  GPDGKPYNNRPVYCTAPCGGQYVSGVYLSPNYPONTYSGQICLYFVTVPPDYVFGQ 1419
      1607  GADGKPSMDALPACQAPCGQYTGSGRGVLSNYPHNTYAGQMCVSTIVPEFVFGQ 1666
      1420  FAFHTALNDVEVDHDSQHSRLSLSGSHTEGSLPLATSNQVLIKFSAGKLAAPARG 1479
      1667  FAFHTALNDVEVDHDSQHSRLSLSGSHTEGSLPLATSNQVLIKFSAGKLAAPARG 1726
      1480  HFVYQAVPRISATQCSSVPEPRYGRKLGSPFSGALYRPECNSGYALQSPLECLPVPG 1539
      1727  HFVYQAVPRISATQCSSVPEPRYGRKLGSPFSGALYRPECNSGYALQSPLECLPVPG 1786
      1540  ALAOMNVASPTCVVPCGNTLBERGTTLSGPEPYLNSLNCWKTIVPFGAGIOTIOVS 1599
      1787  ALAOMNDTITSVVPSCGNTLBERGTTLSGPEPYLNSLNCWKTIVPFGAGIOTIOVS 1846
      1600  FVTEOWNWDSLEVEDGADNTVLMGSPGTTVPALLNSTSNQVLIHFYSDISVSAAGFHL 1659
      1847  FATEOWNWDSLEVEDGADNTVLMGSPGTTVPALLNSTSNQVLIHFYSDISVSAAGFHL 1906
      1660  YKTVGLASSCEPVPVPSNGVYGERLYLVNDVVSQCEBEGVYALQGHANISCMRPGVRRNYP 1719
      1907  YKTVGLASSCEPVPVPSNGVYGERLYLVNDVVSQCEBEGVYALQGHANISCMRPGVRRNYP 1966
      1720  PPLICACGCTVEMEGVILSPGPGVYPPNMCCKVIALPVFGAHIOPLNFSTEBNHD 1779
      1967  SPLICACGCTVEMEGVILSPGPGVYPPNMCCKVIALPVFGAHIOPLNFSTEBNHD 2026
      1780  YIEIRNGPYETSRMGRFSGSELPSLISHTETTVYFHSDBQNRBGFLEYQAVELQ 1839
      2027  YIEIRNGPYETSRMGRFSGSELPSLISHTETTVYFHSDBQNRBGFLEYQAVELQ 2086

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QY 1840 CPDEPANGIVRAGAGVNVGQSVTPECTPEYQUTGHPVLTCOHGTRNMDHPLPKCEVPC 1899
 DB 2087 CPDPAQNGMINDSVGQSSISFECYEGYILGHFVLTCQHGTRNMMVFFPRCDAC 2146
 QY 1900 GGNITSSNGTVSPGSPSSODCWMLTVPIGHGVRLNLSLOTESGPFITMGP 1959
 DB 2147 GYVNTSNGTIVSGPDEYPIKDKMLVTPFGGVYINFTLQTEAVNDYIYVWGP 2206
 QY 1960 QQTAPRLGVFTBMAKTVSSSNQVLLKPHRDATGIFALAFSAVPLTKCPPTILPN 2019
 DB 2207 DQNSPOLGVFSGVNTAETAYSSINQVLLKPHSDFSNGCFVFNFAFQKRCPPRPAPQ 2266
 QY 2020 AAVTNEEFENIDIVRCLPFGTLVGNELTKLGTLOPEGPRLCEVCPNELLT 2079
 DB 2267 ADLTDEDEDEIDFVKYQCHPVTLLSGDILTCKLSOLLFQSSPPTCEACCPANEVRT 2336
 QY 2080 DSGVILSSQSPGSPYQFOTCSMLVNEBDYINISLVEYELSEKQYDEFELPDGSGQSP 2139
 DB 2327 ESSGVILSPQYPGNYENSOQCAMSIKVKENFNITLFDVTFQSEKQFDALFVFDGSGRSP 2386
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 DB 2387 LVLVLSGNTBOSNFTSRNHLXLMSTDHATSKGFKIRYAAPYCSLSTLRNGGILNK 2446
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 RESULT 4
 US-10-016-248-46
 / Sequence 46, Application US/10016248
 / Publication No. US20040033491A1
 / GENERAL INFORMATION:
 / APPLICANT: Alabrook et al.
 / TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
 / FILE REFERENCE: 21402-218
 / CURRENT APPLICATION NUMBER: US/10/016,248
 / PRIOR FILING DATE: 2002-09-20
 / PRIOR APPLICATION NUMBER: 60/254,329
 / PRIOR FILING DATE: 2000-12-08
 / PRIOR APPLICATION NUMBER: 60/291,037
 / PRIOR FILING DATE: 2001-05-15
 / PRIOR APPLICATION NUMBER: 60/255,648
 / PRIOR FILING DATE: 2000-12-14
 / PRIOR APPLICATION NUMBER: 60/297,173
 / PRIOR FILING DATE: 2001-06-08
 / PRIOR APPLICATION NUMBER: 60/309,258
 / PRIOR FILING DATE: 2001-07-31
 / PRIOR APPLICATION NUMBER: 60/326,393
 / PRIOR FILING DATE: 2001-10-01
 / PRIOR APPLICATION NUMBER: 60/315,639
 / NUMBER OF SEQ ID NOS: 167
 / SOFTWARE: Patent In Ver. 2.1
 / SEQ ID NO 46
 / LENGTH: 3508
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 US-10-016-248-46
 Query Match 64.6%; Score 10975; DB 15; Length 3508;
 Beel Local Similarity 62.2%; Pred. No. 0;
 Matches 1912; Conservative 453; Mismatches 592; Indels 118; Gaps 11;
 QY 1 MAGAPPALL-----LPCSLISD-----CCASQNRHSVGVSPSELVKKQILEKRGV 47
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 DB 323 KMLPFSKDSHNSVLSQGVVALVSHVCLDPGLPENRRRAGSDSRKGANVQSSCENYVL 382
 QY 107 QGSKRTICMVSMPFAMSDHPRVPCARMCDAHLRPSGGLTSPNPIIDYDNNACVWII 166
 DB 383 QGSKRTICORVETTLAMSDHRTICARTCGSNLRGPSGVITSPNVPVQYEDNACVWII 442
 QY 167 TALNPKVILAEFEEDLERGYDTLTVGDGDDQDKTVLYMSQNAQSPSPHTPSRIPE 226
 DB 443 TTYDPRKVIKLAEFEELERGYDTLTVGDAGKVGDTIRSLVY-----LTSSVVD 492
 QY 227 ---SMGDIWRQWYVLEICRDISSSDARSGSVKSPKTSNAVELVAPG---TEIEG 278
 DB 493 LTVSMNQWMLH-----LQSDS-----IGSGFKAIVYGEIKG 526
 QY 279 SCGDPIPAYGRREGRFHNGDTLKPECOPAFELVGOKALTCQKNQNSAKKPGCVFSCF 338
 DB 527 GCGDPIPAYGRRTGSSFLHGDTLTFECPAAFEVLGERVITTCQONQNSGNKPSCVFSCF 586

339 FNEFSPGVLSVNYEDYGNHLHCWMLIARPESSRIHLAFNDIDVEPOFDVLIKQAT 398
587 FNTASSGIILSPBYBEYGNMNCWMLIISBPSRHLHFNBDVBPQDFLAVKNGI 646
399 AEAAPVIGTFSGNOLPSSITSSGHVAREFQTDHSTGRKGNITJFTTRHNECDPQVAVN 458
647 SDITVIGTFSGNEVPSQLASSGHIVRLFEQSDHSTGRGNITJFTTQNECHDPGIPIN 706
459 GKRFBDLOLGSSISFLCDEGFLTOGSEITTCVLKAGSVYVANSVAVLRCAPCCGHLTSP 518
707 GRRFGDFLLGSSVSFHCDDGFVYKQSESTICLIDGNVYVMSSTVRCAPCCGHLTAS 766
519 SGITLSPGMPGFYDALSACAWIEPAORGYPKIFTRFTEVNDTLEVDGRTYAPLI 578
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579 GYVHGTQPOLISTSNVYLLFSTDKSHSDIGFOLRYETITLQSDHCLDPGIPVNGORH 638
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639 GNDPVYVALYTFSCDSGITLSDGEPLECEPRFQMSKALPSCCALCGFIOGSSGITLSPG 698
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1007 HTIKAGLFGNFTQVREISDFSMSYEGFNITFSEYDLPECEPEPVAPYSIRKGLQGVGD 1066
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1067 SLTFSCPLGYRLBETAITTCGGRRLMSSPLPFCVACEGNSVTGCTGLSPFPVNYN 1126
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1127 NNHECISIOQOPKGIOLKARAPLESEGVDLYKYDDNNNSARLLAGFSSHEMUGVLYNS 1186
939 TSSSLWDLFTTDAENSTKGFELHPSFELIKCEDPCTPKFGYKXVDEGHPAGSSVSFSCD 998
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1247 PGYAMHGSNTLTCISGDRRWDXPLPFCIAECGQIHAATSGRLSPGYAPAYNNIACHT 1306
1059 WTBABAGCTIGLHFLVFDTEBYVDVLRIMDGPVSEGVLLKELSGPALPMDISTPNSVY 1118
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1607 LGPRGKVVANNRPVCTAPCGGQYVGSDDVYLSNRYQNTTSGQICLYFTVTPVDYVFG 1666
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1787 GALAOMNVSAPTCVVOCGGLTERRGITLSPGPEPLVNSLNCWIKIVVEGAGIOIQV 1846
1599 SFYTEQWMD-SLEVPDADNTVTMLGFSGSGTYPALINSTSNOLYHFDYSDIVSAAGFH 1657
1847 QFCHGABELGPFPIHNGDVTAIRLSFSGTTPALINSTSNOLYHFDYSDIVSAAGFH 1906
1658 LBYKTVGLSCPEPPAVPSNCKTGERYLVNDVVSFOCEPGYALQGHANISCMGTYVRWN 1717
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1718 YPBPCLIAOCGGTVEHEGVILSPGPGNYSMMDCSKIALPVGEGANTOPINSTEPRN 1777
1967 YPBPCLIAOCGGTVEHEGVILSPGPGNYSMMDCSKIALPVGEGANTOPINSTEPRN 2026
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2147 PCGNTTSSNGTYSVSGFPSPYSSODCWLLIVPIGHGRVLLSLIOTEPSSDFTIMD 2206
1958 GPOQTARLGVFTSRMAKKTQVSSNOVLKFRDADATGIPAIAGSAYPLTCCPPTIL 2017
2207 GPOQTARLGVFTSRMAKKTQVSSNOVLKFRDADATGIPAIAGSAYPLTCCPPTIL 2266
2018 PNAEVTEENENIGDIIVRYCLPFTLVGNELITCKLGTLYOPEGPPPICEVHCPTNEL 2077
2267 PNAEVTEENENIGDIIVRYCLPFTLVGNELITCKLGTLYOPEGPPPICEVHCPTNEL 2326
2078 LPTSTGYILSOSYPSIPOTQCSWLVREPDVNIILTYEYPLSEKQYDFEILFDSGQ 2137
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2138 SPLKALSGVYSAPLIYTSNNSVYLRMSSDHAYNKRGFIRYAPYCSLPRAPLHGFIL 2197
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2198 GQTSOPGGSIHFCNAGYRLVGHSMALCTRHOGYHLSMAIPLCOALSGLPEAPKNG 2257
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2378 LPIPNHGRIGTLISYVATAI FSCNSGYTLVGSRYBECMANGLMSGEVYCLAGHCPTPE 2437
2621 LPIPNHGRIGTLISYVATAI FSCNSGYTLVGSRYBECMANGLMSGEVYCLAGHCPTPE 2628
2438 PIVNGHNGENYSGSVYVYQCNAGFRLIGMSVIRICQODHNSGKTPFCVPIICGHPNP 2497
2629 PIVNGHNGENYSGSVYVYQCNAGFRLIGMSVIRICQODHNSGKTPFCVPIICGHPNP 2688
2498 VNGLTQGNFNLDVYVYFVGNPYMAEGARSOCLASGQSDMLPTCRILINCTDPGHQEN 2557

Db 2689 AHGFTNGSEFNLDVNVFTCNTGYLLQGVSRQAQCRSNGQMSPLPTFCRVNCSDEGEVEN 2748
 Qy 2558 SVRGVASHGPHRSFCTTVSYRCNHGFYLLGTPLVSCQDGTWDRBRPOCLVSCGHPGS 2617
 Db 2749 AIHHGQONFESEFEYQMSILYHCKKGFHLGSSALICMANGLMDSLPKCLAIISGHHGV 2808
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 Db 2989 NGIOGTDFTFNKTVSYQCNPGYVMEAVTSATIRCTKGRNPNPKVPKAVLCTQPPPVQ 3048
 Qy 2858 NGKVVSDPMGSSVTVYACLEGYQLSLAVFTCEGNSWTBELPQCFPVFCGDBGVSRG 2917
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 Db 3229 DVRAIDLPFTGYTLV 3243

RESULT 5
 US-10-016-248-47
 ; Sequence 47, Application US/10016248
 ; Publication No. US2004003491A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alabrook et al.
 ; TITLE OR INVENTION: Proteins and Nucleic Acids Encoding Same
 ; FILE REFERENCE: 21402-218
 ; CURRENT APPLICATION NUMBER: US/10/016,248
 ; PRIOR FILING DATE: 2002-09-20
 ; PRIOR APPLICATION NUMBER: 60/254,329
 ; PRIOR FILING DATE: 2000-12-08
 ; PRIOR APPLICATION NUMBER: 60/291,037
 ; PRIOR FILING DATE: 2001-05-15
 ; PRIOR APPLICATION NUMBER: 60/255,648
 ; PRIOR FILING DATE: 2000-12-14
 ; PRIOR APPLICATION NUMBER: 60/297,173
 ; PRIOR FILING DATE: 2001-06-08
 ; PRIOR APPLICATION NUMBER: 60/309,258
 ; PRIOR FILING DATE: 2001-07-31
 ; PRIOR APPLICATION NUMBER: 60/326,393
 ; PRIOR FILING DATE: 2001-10-01
 ; PRIOR APPLICATION NUMBER: 60/315,639
 ; PRIOR FILING DATE: 2001-08-29
 ; NUMBER OF SEQ ID NOS: 167
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 47
 ; LENGTH: 3389
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-016-248-47

Query Match 61.7%; Score 10475.5; DB 15; Length 3389;
 Best Local Similarity 59.9%; Pred. No. 0;

Matches 1843; Conservative 430; Mismatches 565; Indels 237; Gaps 12;
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 Db 383 QGSKSITTCORVETTLAAMDHRPIGRARTCGNLKPSGVITSPNVPQYEDNACVWII 442
 Qy 167 TALNPSKVIKLAFEEDFLERGVDTLTVGQGGDDGOKTYLVMSQACSDSPHTPSRIPE 226
 Db 443 TTTPDPKVIKLAFEELERGVDTLTVGAGKVGSTRSLVY-----LTGSSVVD 492
 Qy 227 ---SNSGDIWRQKWTLLEICRDISSDARSQSVRSPTSNAVELVAPG----TEIRQG 278
 Db 493 LTVSMNQWMLH-----LQSDS-----IGSPGFRAVYQIEIKG 526
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 Db 647 SDITVLTGTFSGNEVPSQASSGHIYRLEFQDHSITTGGEFNIYTFEQNECHDPGPIIN 706
 Qy 459 GKRFGDSLQLGSSISFLCDEGFLTGQSGERTTCYLKXGSVYMNNAVILRCEAPCCGHTSP 518
 Db 707 GRFGDRFLGSSSVSFHDDDFVAKTQGSSEITCLIQGNNVMSSTVRCAPCGHLLAS 766
 Qy 519 SGTILSPWPGPYDALSANVIAOPQYPIKITFDRFKTEVNYDTLEVRDGRYSAPLI 578
 Db 767 SGVILPQWPGYDSDHCEWIIIAKPGHSIKMTFDRFQEVNVDTLEVRDGRASSPLI 826
 Qy 579 GYVHGTQVPCFLISTNVYLLFSTDKSHSDIGQLYRETTITLSDHCLDPGIPVNGQRH 638
 Db 827 GEYHGTQAPOLISTGNFMHLLFTTDSRSSIGLILHYEVSVTLESQCLDPGIPVNGHRH 886
 Qy 639 GNDPYVALVTFSCDSGYTLSDGEPLCEBPNFQMSRALPSCBALCGGFIQSSGTTILSPG 698
 Db 887 GGDGFIIRSTVTFSCDPGYTLSDDEPLVCERNHQNHALPSCDALCGYIQKSGTYLSPG 946
 Qy 699 FPDYPPNNLNCWTWIIETSHKGVFFTRHTHLESCHDYLITNGSFTQPLRQLTGSRLP 758
 Db 947 FPDYPPNNLNCWTWIEVSHKGVQMIPTHTLSSHDYLLITDGGFSFSEVARTLGSVLP 1006
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QY 1059 WTIEBAGCTIGLHFLVDFTEEVVDVLRIMDGPVSGVLLKELSGPALPROLSTFMSVY 1118
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 DB 1907 LEYKTVGLSSCPREPAVNSNGVKTGERLYLVNDVVSFOCEPGVALQGHAIKCMPTVARMN 1966
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 DB 2087 QECDDPEPPANGIVRAGAGVYVQSVTECPGLGYOLTGHPVLTCOHGNRMMDHLPKCEV 2146
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 DB 2147 PCGGINITSNGTVSPGFPBPSYSSQDCVMLITVPPIGHVRLNLSLLQTEBSGDFITIMD 2206
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 DB 2207 GPOQTARLGVFTFSMAKTVQSSNOVLLKFRHDAATGGIFALAEFAYELTKPPTIL 2266
 QY 2018 PNAEVVENEENEFNGIIVRYRCLPGFTLVGNELITCKLGTLOJEBGPPICEVHCPTNEL 2077
 DB 2267 PNAEVVENEENEFNGIIVRYRCLPGFTLVGNELITCKLGTLOJEBGPPICEVHCPTNEL 2326
 QY 2078 LDTSTGVILSQSYGSPQFOTCSMLVREBPNYISLTVFYLSEKQYDEFEIFDGSQ 2137
 DB 2327 RTGSSGVILSPGYGNFNSQTCMSIKVEBNYNIITFVDTFQSEKQFDALLEVVDGSSQ 2386

QY 2138 SPLIKALSGNYSAPLIVTSSNSVYLRWSSDHAYNRKGFRIKRYAPACSLPRAPLHGFIL 2197
 DB 2387 SPLIVLDSNGHTQSNFTSSNOLYLRKMTDHAITSKGFRIKRYAPACSLPRAPLHGFIL 2446
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 DB 2447 NRTAGAVGSKVHYFCKRGMVGHNSNATCRNPLGMQOMDLPPLCOAVCSGIPESPGNG 2506
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 DB 2507 SFTGNBETLDSKVYVCEHBEFGLKSSQQAATAVQOEGLMSNKKRPPCKRVAACPSIEAQL 2566
 QY 2318 VEHGRRELIPETOYQOALMLICDPGYXYTGGQVIRCOANGKMSLSDSTPTCRIISGCE 2377
 DB 2567 SEHVIRLVGSLNIEGAQVLLSCSPGYIEGRRLRCOANGKMTNIDEPSCR----- 2620
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 DB 2621 -----AGHCGSPD 2628
 QY 2438 PIVNGHINGENYRSGSVYVQCNAGRLLIGMSVRICQODHNSGKTPFCVPTICGHPGNP 2497
 DB 2629 PIVNGHISGDFSRVTVVYVQCNPGFRLVGTSVRICLODHKMSGOTPVCPVITICGHPGNP 2688
 QY 2498 VNGLTQONFNLNDVYKFCVNCNPGYMAEGARSOCCLASGOWSDMLPTCRIINTDPPHQEN 2557
 DB 2689 AHGFTNGSEPNLNDVNFCTNCTGYLLOGVSRACRSGNOMSSPLPFCRVNCGSDPGVEN 2748
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 QY 2618 PPHSQNSGDSYTYGAVYRSCIGKRLTVGNSTTMCGLDGHWTSLLPHCSGTSVGVCGDPG 2677
 DB 2809 PANAVALTGEPLFTGAVVHYSCRSSESLIGNDTVECOEDSHMSGALPCTGNPNPGFCGDPG 2868
 QY 2678 IPAHGIRLGDSPDGTVMRPSCEAGHYLRSSERTCOANGSWSGSOEPCGVISCGNPGTP 2737
 DB 2869 TPAHGSRLGDDEFTKSLRPSCEMGHOLKRSPPRTCLINSGWSGLQ----- 2914
 QY 2738 SNARVVSDDLVSASSIYVECREGYVATGLLSRHCNSVNGTWGSDDECLVINGCDPGIPA 2797
 DB 2915 ----- 2914
 QY 2798 NGRLRNDPFRYKNTVYQCVPGTMESHRSVULSTKDRITWNGTKPYCKALMKPPILP 2857
 DB 2915 -----PVCEAVLCPQPPVQ 2929
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 QY 2918 RREDRGFSYRSVSFSCHPPLVYVGSPPRRCQSDGTWGTGOPSICIDPTLLTTCADPGVPOF 2977
 DB 2990 RLSGKSTYKSEVFPQCKSPFLIVGSSRRVCOQADGTWGTGOPSICIDPTLLTTCADPGVPOF 3049
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 DB 3050 GIONNSRGEYVGSVTLFRQCKGYHIOSTTRTCLAMLTWGTGOTECIPHACROPEPTTHA 3109
 QY 3038 NVGALDLPBWSGYLLI 3052
 DB 3110 DVRAIDLPRTGYTLV 3124

RESULT 6
 US-10-408-765A-2286
 ; Sequence 2286, Application US/10408765A
 ; Publication No. US20040101874A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ghosh, Soumitra S.
 ; APPLICANT: Fahy, Boia D.
 ; APPLICANT: Zhang, Bing


```

APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Martone, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2286
LENGTH: 3389
TYPE: PRT
ORGANISM: Homo sapiens
US-10-408-765A-2286

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Query Match 61.7%; Score 10475.5; DB 16; Length 3389;
Best Local Similarity 59.9%; Pred. No. 0;

Matches 1843; Conservative 430; Mismatches 565; Indels 237; Gaps 12;

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QY 48 KLMPKSDNSQKTSVLTQVGVSGHNMCPDPCIPEKRGKLGSDF-RLGSSVQFTCNBEGYDL 106
DB 332 KMLPKSDGSHKNSVLSQGVVALVSHMCLDPCIPEKRGAGSDPFRVGNANVOFSCEDNYVL 382
QY 107 QGSKRITOMKYSDMAAMSDHRRPVRCAMCAHLRGPSSGITSNPFLOYDNNAHCWII 166
DB 303 QGSKRITOMKYSDMAAMSDHRRPVRCAMCAHLRGPSSGITSNPFLOYDNNAHCWII 442
QY 167 TALNPKYIKLAFEEFDLERYGDTLTVGGDGDQDKTVLYMSQNASDSDPHRPGSIPE 226
DB 443 TTTPDVKYIKLAFEEFDLERYGDTLTVGGDGDQDKTVLYMSQNASDSDPHRPGSIPE 492
QY 227 ---SMGSGIMQKTVLEICRDISSDARSVSKSPKTSNAVELVAPG-----TEIEQG 278
DB 493 LIVSNMOMLH-----LQSDDS-----ISPGFKAVYQIEBK 526
QY 279 SCGDPGIPAYGRGSRFHGDTLKFECOPAFELVQKAITCOKNOMSAKRCGCVSP 338
DB 527 GCGDPGIPAYGRGSRFHGDTLKFECOPAFELVQKAITCOKNOMSAKRCGCVSP 586
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DB 647 SDIVLATIFSGNEVPQLASSGHIKRLFEQSDHSTTGRGNITVYTFQNECHDPIGIN 706
QY 459 GKRFGLQLQSSISFLCDGFLATQGSFETITCVLKEGSAVMNSAVLARCCEACGGLTSP 518
DB 707 GRFRGDFLLGSSVFFHCDGFLATQGSFETITCVLKEGSAVMNSAVLARCCEACGGLTSP 766
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DB 827 GEVHGQAPQFLISTSNVLYLFTSTKSHSDIGFOLRYETITLQSHCHLDPITPNQGRH 886
QY 639 GNPFIYCALVTFSCDGYTLSDDEPLECEPNFOWSRALPSCBALCGGFIQSSGTTILSPG 698
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QY 699 FPDFYNNINCTWIIITSHGKGVFFRHHLESGHDIYLLITENSGSFQOPLQTLGSLP 758
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DB 1907 LEYKTVGLSSCPPEAVPSNGVKTGERVYLVNDVVSFOCEEGVALOGHAHISCMPTGTRRN 1966
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2147 PCGNTVTSQNGTIVSPGFPDEYPIIKDCIMLITVPBGHGVYINFTLLQTEAVNDYIAVMD 2206
1958 GPGOTAPRLGVFRSMKKTVOSSSNVILKPHNDATGGIPIAFSAAYLTCCPPTIL 2017
2207 GPDONSQOLGVFSGNTALETVASTNOVLLKPHSDFNSNGFVNLNFAFQKCKQPPAV 2266
2018 PNAEVVTESEFNIGDIIVRYRCLPGFTLVGNEILTCKLTGYLOFEPPICEVHCPTNEL 2077
2267 PQAMELDEDDDEFIDGVKQCHRGYTLVGTDLTCKLSSQLOFEGSLPTCEAQCPANEV 2226
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2378 LPIPNHGRIGTSLVYGATAIFSCNSGYTLVGSFVRRCMANGLWSGSEVNLCAHGCSPB 2437
2621 -----AGHCSPD 2628
2438 PIVNGHINGENYSTRGVVYOCNAGFRILGMSVRIICQODHHMSKTPPCVPITCGHPNP 2497
2629 PIVNGHISGDFSRDPTVVVQCNGFRLVGTSVIRICLQDHMSQGTVCVPITCGHGNP 2688
2498 VNGLTQONOPNLNVKFCNPGMGMAAARSQCLASGOWSDMLPTCRINIICNDPQHON 2557
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2749 AIRHGQONFPESFEYGMSTLYHCKKGRHLGSSALITCMANGMLNRSIPKCLATISGHPGV 2808
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2809 PANAVLTGELPTYGAVVHYSCRGSESLIGNDTRVCOEDSHMSGALPHCTGNNPFGCDDPG 2868
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2915 ----- 2914
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2915 -----PVCEAVLCPQPPVQ 2929
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2930 NGTEGSDFRWGSISYSQMDGYOLSHALISCEGRGWKEISIPQCLPVEFGDGIABEG 2989
2918 RREDRGFSYRSVSFSCHPPLVLVGSPPRFQSDGTGSGTOPSCIDPLTTCADPGVQF 2977

Db 2990 RLSGKSFYKSEVFFOCKSEFLLVGSRRVCAQDGTWSGIOPTCIDPAHNTCPDGPMPH 3049
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Db 3050 GIONSSRGYEVSGTVFPRCKGYHIGSTTRCLANLWTSIGIOTECIPHACRPEPTPAH 3109
Qy 3038 NVGALDLPMSGYTLI 3052
Db 3110 DVRAIDLPTFGYTLV 3124
RESULT 7
US-10-467-433-18
; Sequence 18, Application US/10467433
; Publication No US2004008773A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION;
; APPLICANT: LAL, Preeti G.; BAUGHN, Mariah R.;
; APPLICANT: YAO, Monique G.; CHAWLA, Narinder K.;
; APPLICANT: ELLIOTT, Vicki S.; XU, Yuming;
; APPLICANT: HONCHELL, Cynthia D.; YUE, Henry;
; APPLICANT: DING, Li; GIETZEN, Kimberly J.;
; APPLICANT: ISON, Craig H.; LU, Dyung Aina M.;
; APPLICANT: HAFALIA, April J.A.; GANDHI, Ameena R.;
; APPLICANT: THANGAVELU, Kavitha; SANJANMALA, Madhusudan M.;
; APPLICANT: TANG, Y. Tom; RAMKUMAR, Jayalaxmi;
; APPLICANT: GRIFFIN, Jennifer A.; SMARNAKAR, Anita;
; APPLICANT: AZIMZAI, Yaida; SAPPERSTEIN, Stephanie K.;
; APPLICANT: BURFORD, Neil; LEE, Ernestine A.;
; APPLICANT: LU, Yan; TRAN, Uyen K.;
; APPLICANT: MAROUIS, Joseph P.
; TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT
; FILE REFERENCE: PF-0899 USN
; CURRENT APPLICATION NUMBER: US/10/467,433
; PRIOR APPLICATION NUMBER: 2003-08-06
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/US02/03709
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/266,117
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/269,618
; PRIOR FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: US 60/271,118
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: US 60/274,486
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 60/274,436
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 60/334,229
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/353,284
; PRIOR FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PERL Program
; SEQ ID NO 18
; LENGTH: 1958
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 55061615CD1
US-10-467-433-18
Query Match 53.1%; Score 9025.5; DB 15; Length 1958;
Best Local Similarity 86.4%; Pred. No. 0;
Matches 1692; Conservative 3; Mismatches 6; Indels 257; Gaps 8;
Qy 892 GKGIOKARAFELISEGVDLVKYVDGNNNSARLLGVFHSBEMGYTLNSTSSLMJDFITDA 951
Db 15 GKRIQLKARAFELISEGVDLVKYVDGNNNSARLLGVFHSBEMGYTLNSTSSLMJDFITDA 74
Qy 952 ENTSKGFELHFSFELIKCEDPGTPKRGYKVDHGHFAGSSVSFSCDPGYSLRGSEBLIC 1011
Db 75 ENTSKGFELHFSFELIKCEDPGTPKRGYKVDHGHFAGSSVSFSCDPGYSLRGSEBLIC 134

QY 1012 LSGERRTWBPLPTCYAECGGTVRGVSGOVLSPGPAPYENHNCITWTEACCTIGL 1071
 DB 135 LSGERRTWBPLPTCYAECGGTVRGVSGOVLSPGPAPYENHNCITWTEACCTIGL 194
 QY 1072 HELVPTDEEVDLRIWDPVSESVGLLKEJSGPALPKDLHSTFNSVLOFSTDFSTSGOG 1131
 DB 195 HFLVPTDEEVDLRIWDPVSESVGLLKEJSGPALPKDLHSTFNSVLOFSTDFSTSGOG 254
 QY 1132 FALQFVSTATSCNDGIPONGSRGSDSWEADSTVFOCDPGVALQSGAEISCVKIENRF 1191
 DB 255 FALQFVSTATSCNDGIPONGSRGSDSWEADSTVFOCDPGVALQSGAEISCVKIENRF 314
 QY 1192 FMOQSPPTCIAPCGGDLTSPGVILSPNYPPEYPPGCKEDMKVTYSPDYVALVFNPNL 1251
 DB 315 FMOQSPPTCIAPCGGDLTSPGVILSPNYPPEYPPGCKEDMKVTYSPDYVALVFNPNL 374
 QY 1252 EBGYDPLHLYDGRDLSPLIGSFYGSOLPGR1ESSNSLFLAFRSDASVSNAGFYIDYTE 1311
 DB 375 EBGYDPLHLYDGRDLSPLIGSFYGSOLPGR1ESSNSLFLAFRSDASVSNAGFYIDYTE 434
 QY 1312 NPRESCFDEGSIKNGTRVSGDLKLGSSVTVYCHGGEVEGTSLSCLIGPDKGKWMNPR 1371
 DB 435 NPRESCFDEGSIKNGTRVSGDLKLGSSVTVYCHGGEVEGTSLSCLIGPDKGKWMNPR 494
 QY 1372 PVTCTAPCGGQYVSGDGVILSPNYPONTSGOICLYFVTVPRDYVFGQPAFFHTALNDVY 1431
 DB 495 PVTCTAPCGGQYVSGDGVILSPNYPONTSGOICLYFVTVPRDYVFGQPAFFHTALNDVY 554
 QY 1432 EVDHDSHOSRLLSLSSGSHT----- 1452
 DB 555 EVDHDSHOSRLLSLSSGSHT----- 614
 QY 1453 ----- 1452
 DB 615 CLSCGACTQRSSQOLVRAPTSGAFSSCPHPDCVYTAFLMCSLLLNNGNTMNLQOVLVS 674
 QY 1453 ----- 1480
 DB 675 LPMWICTAPSRRTYFVFCYKSCOSTLVSCAHAGSLPLATSNOL1KFSAKGLAPARGFI 734
 QY 1481 FVYQ-----AVPRTSATOCSSVPEPRYKRLGSPFSGALVREPCNSGVYALQSPFI 1532
 DB 735 FVYQMEDMDAGAVPRTSATOCSSVPEPRYKRLGSPFSGALVREPCNSGVYALQSPFI 794
 QY 1533 ECLFVPBALAOMNVSAPTCVPPCCGNTLERRGTTLSFGPEPYLNSLNCWKIIVDEGAG 1592
 DB 795 ECLFVPBALAOMNVSAPTCVPPCCGNTLERRGTTLSFGPEPYLNSLNCWKIIVDEGAG 854
 QY 1593 IOIQVVSFVTEBQWMDSLFVFDGADNTVTLGSPSGTTPPALNSTNOULYHFYSITS 1652
 DB 855 IOIQVVSFVTEBQWMDSLFVFDGADNTVTLGSPSGTTPPALNSTNOULYHFYSITS 914
 QY 1653 AAGHLEYKTVGLSSCEPAPVPSNGVYTGERYLVNDVVSFOCEPGYALQGAHISCMPT 1712
 DB 915 AAGHLEYKTVGLSSCEPAPVPSNGVYTGERYLVNDVVSFOCEPGYALQGAHISCMPT 974
 QY 1713 VRBNVYPPPTCIAQCGGTVEMEGVILSPFPENYNSMDCSKWIALPVFGAHIOPLNF 1772
 DB 975 VRBNVYPPPTCIAQCGGTVEMEGVILSPFPENYNSMDCSKWIALPVFGAHIOPLNF 1034
 QY 1773 STEPNHDIYERINNGPYETSRMGRFGSELPSLSLSTSHETTVYHSHDSQNRPFKLEY 1832
 DB 1035 STEPNHDIYERINNGPYETSRMGRFGSELPSLSLSTSHETTVYHSHDSQNRPFKLEY 1094
 QY 1833 Q-----AYELOCEPDPEPFANGI 1850
 DB 1095 QDLTYHQJSSFLRGDLSELERTNSTPVAASYWMDLDPCECAEYELQCEPDPEPFANGI 1154
 QY 1851 VRGAGYVNGQSVTFECLPGYQLTGHPVLTCQGTNRNDMHP1PKREVCCGNTSSNTV 1910
 DB 1155 VRGAGYVNGQSVTFECLPGYQLTGHPVLTCQGTNRNDMHP1PKREVCCGNTSSNTV 1214

QY 1911 YSPGFPYSSSODCWLITV-PIGHVRLNLSLQTEPSGDEITIMDGPQOTAPRLGVF 1969
 DB 1215 YSPGFPYSSSODCWLITVQNLAMGVRLNLSLQTEPSGDEITIMDGPQOTAPRLGVF 1274
 QY 1970 TRSMAKTVOSSNOVLKFRHDATGFI PAIAFSAVPLTKCPPTILPNAEVTENEBF 2029
 DB 1275 TRSMAKTVOSSNOVLKFRHDATGFI PAIAFSAVPLTKCPPTILPNAEVTENEBF 1334
 QY 2030 NIGDIYRCLPGFTLVGNELTCKLGTLOEGEPPTICEVHCPTMELLTDSGTVILSOS 2089
 DB 1335 NIGDIYRCLPGFTLVGNELTCKLGTLOEGEPPTICEVHCPTMELLTDSGTVILSOS 1394
 QY 2090 YPGSTYQFOTCSMLVREPDYNI SLTVEYFLSEKQYDEBEIPDGSGOSPILKALSGNVS 2149
 DB 1395 YPGSTYQFOTCSMLVREPDYNI SLTVEYFLSEKQYDEBEIPDGSGOSPILKALSGNVS 1454
 QY 2150 APLIYVSSNSVYLRMSDHAHNRGPFTRYSAPICSLPRABLHGFILQSTOPGSIH 2209
 DB 1455 APLIYVSSNSVYLRMSDHAHNRGPFTRYS-----GOTSTOPGSIH 1498
 QY 2210 FCGNAGYRLVGHSMALCTRHPOGYHLMSEALPLCOALSCLPAPKNGVFGKXTVGTX 2269
 DB 1499 FCGNAGYRLVGHSMALCTRHPOGYHLMSEALPLCOALSCLPAPKNGVFGKXTVGTX 1558
 QY 2270 AVYSGSEGYHQAQAEATACELDTGLMSNRVPPQCV-----PYTCDVSSISVEH 2320
 DB 1559 AVYSGSEGYHQAQAEATACELDTGLMSNRVPPQCVRESGNGGAVTCDVSSISVEH 1618
 QY 2321 GWRMLIFETOYQFOQLMLICDPGYVYTGORVITCOANAKSLDSTPTCCIIISCGELPI 2380
 DB 1619 GWRMLIFETOYQFOQLMLICDPGYVYTGORVITCOANAKSLDSTPTCCIIISCGELPI 1678
 QY 2381 PBNGRIRITLSYGTATAFSCNSGYTLVGSVRECMANGLSGSEVRL----- 2429
 DB 1679 PBNGRIRITLSYGTATAFSCNSGYTLVGSVRECMANGLSGSEVRL----- 1738
 QY 2430 -----AGHCGTEPIVNGHINENSVYSGVYVQCNAPFRLIGNSVRIICOQ 2475
 DB 1739 KULFVYSSPSLTYRAGHCGTEPIVNGHINENSVYSGVYVQCNAPFRLIGNSVRIICOQ 1798
 QY 2476 DHMSGKTPFCV-----PITGHPGNVNLTOGNQPNLN 2510
 DB 1799 DHMSGKTPFCVHQOQLLLLLLLCCDDDDDEDDGSAICGHGPNVNLTOGNQPNLN 1858
 QY 2511 DVVFVNCNPGYMAAGARSOCCLASGOWSMLPTCRIINCTDPOHNSVROVHAGSHRF 2570
 DB 1859 DVVFVNCNPGYMAAGARSOCCLASGOWSMLPTCRIINCTDPOHNSVROVHAGSHRF 1918
 QY 2571 SFGTTVSYRCNHGFYLLGTIVLSQCGDGTWDRRPQCL 2608
 DB 1919 SFGTTVSYRCNHGFYLLGTIVLSQCGDGTWDRRPQCL 1956

RESULT 8
 US-10-276-934-13
 ; Sequence 13, Application US/10276934
 ; Publication No. US20030180750A1
 ; GENERAL INFORMATION:
 ; APPLICANT: University of Leeds
 ; APPLICANT: Markham, Alexander F.
 ; APPLICANT: Jackson, Andrew P.
 ; TITLE OF INVENTION: Treatment of Cancer and Neurological diseases
 ; FILE REFERENCE: 9052-144
 ; CURRENT APPLICATION NUMBER: US/10/276, 934
 ; PRIOR FILING DATE: 2002-11-20
 ; PRIOR APPLICATION NUMBER: PCT/GB01/02240
 ; PRIOR FILING DATE: 2001-05-21
 ; PRIOR APPLICATION NUMBER: GB0012186.3
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 13

LENGTH: 2352
TYPE: PR1
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (11)..(11)
OTHER INFORMATION: "x" is unknown amino acid
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (212)..(212)
OTHER INFORMATION: "x" is unknown amino acid
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (594)..(594)
OTHER INFORMATION: "x" is unknown amino acid
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (731)..(731)
OTHER INFORMATION: "x" is unknown amino acid
US-10-276-934-13

Query Match 45.1%; Score 7662.5; DB 14; Length 2352;

Best Local Similarity 65.7%; Pred. No. 0;
Matches 1357; Conservative 291; Mismatches 341; Indels 77; Gaps 11;

1 MAGAPPALC-----LPCSLISD-----CCASNRHSVSGVPSSELVKQIELKRGV 47
310 ISGTEBBSIMWTGNLSPVSSKNWLRHFTSDSNHRK-GFNAQFQVKALIELKRGV 368
48 KLMPKSNQKTSVLTQVVSQGHMCPDPCI PERGKRLGSDPFLGSSVQFTCEGYDLQ 107
369 KMLPSKDSKSHKNSVLSQGVVALVSDMCPDPCI PENGRASDPRFVGNVQSSCDNVTLO 428
108 GSKKITCKKTSMDMAANSDBRPVCRAMCAHLGPGSIIITSPNPIQYNNACWIIIT 167
429 GSKKITCKKTSMDMAANSDBRPVCRAMCAHLGPGSIIITSPNPIQYNNACWIIIT 488
168 ALNRSKVIKLAFFEEFDLERGYDTLVGCGGODGOKTLYVMSQACDSPTHTPSRIPE- 226
489 TTDDKVIKLAFFEEFDLERGYDTLVGCGGODGOKTLYVMSQACDSPTHTPSRIPE- 538
227 --SNSGDIWROKMTVLEICRDISSDARSQSVKSPKTSNAVELVAPG---TEIRGS 279
539 IVSMNSQMLH-----LQSDS-----IGSPGFAXVQEIIRKG 572
280 CGDPGICAYGRBBSRHHGDTLKFECOPAFELVQKAITCQKNQSAKKPGCVFSCFP 339
573 CGDPGICAYGRBBSRHHGDTLKFECOPAFELVQKAITCQKNQSAKKPGCVFSCFP 632
340 NFPSPGCVLSPNYPEDYGNHLHCVLILAPESRIHLAFNDIVEPQDPFLVTKDQATA 399
633 NFPSPGCVLSPNYPEDYGNHLHCVLILAPESRIHLAFNDIVEPQDPFLVTKDQATA 692
400 EAPVLTGTFSGNQLPSSITSSGVARLEFQTHSTGKGFNITFTFRHNECPDGVNPG 459
693 DITVLTGTFSGNQLPSSITSSGVARLEFQTHSTGKGFNITFTFRHNECPDGVNPG 752
460 KRPEDSLQSSSIFLCEGFLGTQSGFTITCVLKEGSVWNSAVLRCAPCGHITSPS 519
753 KRPEDSLQSSSIFLCEGFLGTQSGFTITCVLKEGSVWNSAVLRCAPCGHITSPS 812
520 GTLSPMPGPFYKALSCAWIEAOGPYKITFEDRFTENYVTLVRODRYTSAPLIG 579
813 GTLSPMPGPFYKALSCAWIEAOGPYKITFEDRFTENYVTLVRODRYTSAPLIG 872
580 VYHGTQVQPLISTSNVLYLFTDQSHSDIGFOLRYETITLQSDHCLDPGI PVNGORHG 639
873 EYHGTQVQPLISTSNVLYLFTDQSHSDIGFOLRYETITLQSDHCLDPGI PVNGORHG 932
640 NDFVYVGLVLTSCSGITLSDGEPLECPNFQMSRALPSCALCGGFIQSSSGTILSPGF 699
933 GDFGIRSTVTFSCDPGYTLSDDEPLVCRNHQNMHALPSCALCGGYIQGSGTILSPGF 992

QY 700 PDFYNNINACTWIIETSHGKGVFTFTFTPHLESGBDYLITENGSFTQPLROLTGRSLPA 759
DB 993 PDFYNNINACTWIIETSHGKGVFTFTFTPHLESGBDYLITENGSFTQPLROLTGRSLPA 1052
QY 760 PISAGLYGNFTAOVRPISDFSMVYEGNITFSEYDLEPCEPEVPAVSIRKGLQFVGDT 819
DB 1053 TIRAGLGNFTAOVRPISDFSMVYEGNITFSEYDLEPCEPEVPAVSIRKGLQFVGDT 1112
QY 820 LTFSCFPGRVLEGRARTICGRRRLMSSRLPCVACGNSVYCTOCTLLSPNPNVYN 879
DB 1113 LTFSCFPGRVLEGRARTICGRRRLMSSRLPCVACGNSVYCTOCTLLSPNPNVYN 1172
QY 880 NHECTIYIOTOPGKGIOLKARAFELSGDYLYKYDGNNSARLLGVSHSEMMGVINST 939
DB 1173 NHECTIYIOTOPGKGIOLKARAFELSGDYLYKYDGNNSARLLGVSHSEMMGVINST 1232
QY 940 SSSLMLDPTIDAENTSKEFLHFSFELICEDEPGTPKFGYKYHDEGHFAGSSVSFSCDP 999
DB 1233 SSSLMLDPTIDAENTSKEFLHFSFELICEDEPGTPKFGYKYHDEGHFAGSSVSFSCDP 1292
QY 1000 GYSLRGEELLCSGERRTWDRPLPTCVACCGTVAGSVOYLSPCGYAPYENHNCIW 1059
DB 1293 GYSLRGEELLCSGERRTWDRPLPTCVACCGTVAGSVOYLSPCGYAPYENHNCIW 1352
QY 1060 TIEAAGCTTGLHFLVPTDEVDVLRIMDPVSGVLYKELSGPALPKDLHSTFNSVL 1119
DB 1353 TIEAAGCTTGLHFLVPTDEVDVLRIMDPVSGVLYKELSGPALPKDLHSTFNSVL 1412
QY 1120 QFSTDFTSKQGAIOFVSSTATSCNDPCI PONGSRSGDSWEAGDSVTFQCDPGYALQS 1179
DB 1413 QFSTDFTSKQGAIOFVSSTATSCNDPCI PONGSRSGDSWEAGDSVTFQCDPGYALQS 1472
QY 1180 AETSCKIENRFPQSPPTCIAACGGDLTGPBGVILSPNYPERYPKCKDMKVTYVSPD 1239
DB 1473 AETSCKIENRFPQSPPTCIAACGGDLTGPBGVILSPNYPERYPKCKDMKVTYVSPD 1532
QY 1240 YVALVFNINFLERGVYFLIYDGRDLSPLIGSFYSGQIPGRITSSNSLFLAFRSDAS 1299
DB 1533 YVALVFNINFLERGVYFLIYDGRDLSPLIGSFYSGQIPGRITSSNSLFLAFRSDAS 1592
QY 1300 VSNAGFVIDYTERPESCFDPGSIKNGTRVSGDLKLGSSVYVYCHGGEVEGTSTLCL 1359
DB 1593 VSNAGFVIDYTERPESCFDPGSIKNGTRVSGDLKLGSSVYVYCHGGEVEGTSTLCL 1652
QY 1360 GPDPKPYWNNRPVCTAPCCGGYVGSNGVILSPNYPONTYSGQICLYFVVPVDPYVFCQ 1419
DB 1653 GPDPKPYWNNRPVCTAPCCGGYVGSNGVILSPNYPONTYSGQICLYFVVPVDPYVFCQ 1712
QY 1420 FAFPHTLNINVEVHDGSHSRLSLSGSHGESLPLATSNQVLKIFSAKGLAPARGF 1479
DB 1713 FAFPHTLNINVEVHDGSHSRLSLSGSHGESLPLATSNQVLKIFSAKGLAPARGF 1772
QY 1480 HFVYQAVPRTSATQSSVPEPRYKRLGSDFSVGAIVFPCNSGYALQGSPEIECLVPG 1539
DB 1773 HFVYQAVPRTSATQSSVPEPRYKRLGSDFSVGAIVFPCNSGYALQGSPEIECLVPG 1832
QY 1540 ALAQMNSAATCVYPCCGNLTERRGTLISGFPFPPYINSLNCTWKIYVPGAGIQTIOVS 1599
DB 1833 ALAQMNSAATCVYPCCGNLTERRGTLISGFPFPPYINSLNCTWKIYVPGAGIQTIOVS 1892
QY 1600 FVTEQWMSLEVPDGAINTVTLGSGFTVPLALNISTSNQLYLHFYSDISVSAAGFHL 1659
DB 1893 FVTEQWMSLEVPDGAINTVTLGSGFTVPLALNISTSNQLYLHFYSDISVSAAGFHL 1952
QY 1660 YKTIVGLSSCEPAVPSNGVYGERIYLVNDVVSFOCEBGVALQGHAIISMPGVYRNVYP 1719
DB 1953 YKTIVGLSSCEPAVPSNGVYGERIYLVNDVVSFOCEBGVALQGHAIISMPGVYRNVYP 2012
QY 1720 PPLCIAOCGGTVEBMEVILSPGPGYVPSNMCMKIALPVGRGAIIOFLNSTERNHD 1779
DB 2013 PPLCIAOCGGTVEBMEVILSPGPGYVPSNMCMKIALPVGRGAIIOFLNSTERNHD 2072
QY 1780 YIEIRNPFYETSRMGAFSGSELPSLLSTSHETTVYFHSDHQNRPGLKLEYQAYELQE 1839

Db 2073 FLEIQNGPYHTSMIGOFSGTDLPAALSTHETLHFDSDSQNRGFKLAYQAYELON 2132
 Qy 1840 CPDPEFANGIVGAGAVNIGOSTFECLEGYOLTGHPVLTCHGNRMWHPDPRCEVPC 1899
 Db 2133 CPDPEFANGIVGAGAVNIGOSTFECLEGYOLTGHPVLTCHGNRMWHPDPRCEVPC 2192
 Qy 1900 GGNITSSNGTVSPGFPSPYSSODCVMLITVPIGHVRLNLSLQTEPSGDFITIMGP 1959
 Db 2193 GYVVTSONGTIVSPGFPDEYPLIKOCIMLITVPHGVYINFTLQTEAVNDYLAWMDGP 2252
 Qy 1960 QGTAPRLGVFTSMMAKTYQSSNOYLLKFRDAAATGIFALAFSAV-----PLTK----- 2010
 Db 2253 DONSQOLGVFSNTALLETAYSSSTNOYLLKFRHSDFSNGGFFVLNPHGOLITPPLVXTENS 2312
 Qy 2011 -----CPPP-----TILPVAEVTEN 2026
 Db 2313 WCLLOCCPFPQFLKFLDSAGSVDS 2338

RESULT 9
 US-10-276-934-14
 ; Sequence 14, Application US/10276934
 ; Publication No. US20030180750A1
 ; GENERAL INFORMATION:
 ; APPLICANT: University of Leeds
 ; APPLICANT: Markham, Alexander F.
 ; APPLICANT: Jackson, Andrew P.
 ; APPLICANT: Woods, Christopher G.
 ; TITLE OF INVENTION: Treatment of Cancer and Neurological Diseases
 ; FILE REFERENCE: 9052-144
 ; CURRENT APPLICATION NUMBER: US/10/276, 934
 ; PRIOR FILING DATE: 2002-11-20
 ; PRIOR APPLICATION NUMBER: PCT/GB01/02240
 ; PRIOR FILING DATE: 2001-05-21
 ; PRIOR APPLICATION NUMBER: GB0012186.3
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 14
 ; LENGTH: 2306
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: MISC FEATURE
 ; LOCATION: (166)..(166)
 ; OTHER INFORMATION: "X" is unknown amino acid
 ; FEATURE:
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 ; OTHER INFORMATION: "X" is unknown amino acid
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 ; LOCATION: (685)..(685)
 ; OTHER INFORMATION: "X" is unknown amino acid
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 ; LOCATION: (1013)..(1013)
 ; OTHER INFORMATION: "X" is unknown amino acid
 ; US-10-276-934-14

Query Match 45.0%; Score 7643.5; DB 14; Length 2306;
 Best Match Similarity 65.6%; Pred. No. 0;
 Matches 1355; Conservative 290; Mismatches 344; Indels 77; Gaps 11;

Qy 1 MAGAPPALI-----LPCSLISD-----CCASQNRHSVGVGPSELVYKQJELKSRGV 47
 Db 264 ISGTETAPSIWLTGMNLPSPVSISSKNWLRHFTSDSHRRK-GNNAPQVYKKAIELKSRV 322
 Qy 48 KLMPKDNOSKXTVLTVQVSGSHNCCPDPGIPEKRLGSDPRLLSSVQFTCNESYDIQ 107
 Db 323 KLMPKDNOSKXTVLTVQVSGSHNCCPDPGIPEKRLGSDPRLLSSVQFTCNESYDIQ 382
 Qy 108 GSKRITCMKVSDFMAASDHRPVCARMCDAHLRGSGIITSPNPIQYDNNACWIIIT 167
 Db 383 GSKRITCMKVSDFMAASDHRPVCARMCDAHLRGSGIITSPNPIQYDNNACWIIIT 442
 Qy 168 ALMPKSVITKLAPFEPLENGYDTLTVGDCGQDQKTVLYMSQNASDPSHTPGSRIP- 226
 Db 443 TTPDQVYIKLAXEPELENGYDTLTVGDCGQDQKTVLYMSQNASDPSHTPGSRIP- 492
 Qy 227 --SMSGDIWROKWTVLICRDISSPARAGSRKSPKISNAELVAPG-----TIEQGS 279
 Db 493 IYMSKNQMLH-----LQSDDS-----ISPGKAYOIEIKGG 526
 Qy 280 CGDPGIPAYGRBEGSRFHHGDTLKECPAPFELVGOKAITCQKNNQMSAKKPGCVFSCPF 339
 Db 527 CGDPGIPAYGRBEGSRFHHGDTLKECPAPFELVGOKAITCQKNNQMSAKKPGCVFSCPF 586
 Qy 340 NFTPSPGVVLSPNYEDYDGNHLCWILLAPRESIHLAFNDIDYEPQDFLVIQGATA 399
 Db 587 NFTPSPGVVLSPNYEDYDGNHLCWILLAPRESIHLAFNDIDYEPQDFLVIQGATA 646
 Qy 400 EAPVLGTPESGNDLPSSITSGHVARLEFQDHTSTKRGFNITFTFRINCEGDPVPVNG 459
 Db 647 DITVLTGTFSGNVEPQLASSGHIVALEFQDHTSTKRGFNITFTFRINCEGDPVPVNG 706
 Qy 460 KRGDSLOGSSISLCEBGLTGQSGEITTCVLEKGSVNNASAVLRCEADCGHLLTSPS 519
 Db 707 KRGDSLOGSSISLCEBGLTGQSGEITTCVLEKGSVNNASAVLRCEADCGHLLTSPS 766
 Qy 520 GTILSPGMPGFYKDALSCAWYEAOPGVPIKITDRPFTENVYDTLEVRDERTSAPLIG 579
 Db 767 GTILSPGMPGFYKDALSCAWYEAOPGVPIKITDRPFTENVYDTLEVRDERTSAPLIG 826
 Qy 580 VYHGTQVQFLISTSNVLYLLPSTDKSHSDIGQLRYETITLQSDHCLDPGIPVNGORHG 639
 Db 827 EYHGTQVQFLISTSNVLYLLPSTDKSHSDIGQLRYETITLQSDHCLDPGIPVNGORHG 886
 Qy 640 NDFYVYALVTFSCDQSGVTLSDGEPLCEPNQWRALPSCGALCGGRTIOGSGITLSPGF 699
 Db 887 GDFGIRSTVTFSCDQSGVTLSDGEPLCEPNQWRALPSCGALCGGRTIOGSGITLSPGF 946
 Qy 700 PDFYVYALVTFSCDQSGVTLSDGEPLCEPNQWRALPSCGALCGGRTIOGSGITLSPGF 759
 Db 947 PDFYVYALVTFSCDQSGVTLSDGEPLCEPNQWRALPSCGALCGGRTIOGSGITLSPGF 1006
 Qy 760 PISAGLVNFTPAQVRFISDSMSGEGNITFSEYDLPECEPEVPAVSIRKGLQFGVGD 819
 Db 1007 PISAGLVNFTPAQVRFISDSMSGEGNITFSEYDLPECEPEVPAVSIRKGLQFGVGD 1066
 Qy 820 LTFSCFPYRLGEGTARITLCGGRRLWSSPLPCVAVCGNSVTGCTGLSPNPNVYNN 879
 Db 1067 LTFSCFPYRLGEGTARITLCGGRRLWSSPLPCVAVCGNSVTGCTGLSPNPNVYNN 1126
 Qy 880 NHECIYSIQTPQKGIQKLKARAFELSEGDVLYKYDGNNSARLLGVFSHNNAGVTLNST 939
 Db 1127 NHECIYSIQTPQKGIQKLKARAFELSEGDVLYKYDGNNSARLLGVFSHNNAGVTLNST 1186
 Qy 940 SSSLMLDFITDAENTSGPELHSSSELLKCEBPGTPKPGKYKXHDGHRAGGSVFSQCDP 999
 Db 1187 SSSLMLDFITDAENTSGPELHSSSELLKCEBPGTPKPGKYKXHDGHRAGGSVFSQCDP 1246
 Qy 1000 GYSLRGSSEELLCGSRRTWRDLPTCVABCGTAVGEVSGVLYSGYVAPYVHNHNCJM 1059
 Db 1247 GYSLRGSSEELLCGSRRTWRDLPTCVABCGTAVGEVSGVLYSGYVAPYVHNHNCJM 1306
 Qy 1060 TIRAEAGCTTGLHFLVFTBEVHVDLRIWDGPVESVLLKELSGPALPKDLHSTFNSVVL 1119

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1307 IIEADPGTISLHFIIVFOTEMAHDILKWMGDVPDSDILKXMSGALPEDIHSTFNSITL 1366
1120 QFSDFPFSKGFALIOFSVSTATSCNDGIPONSRSRSDSHEADSTVFQCDPGYALQGS 1179
1367 QFDSDFPFSKGFALIOFSVSTATSCNDGIPONSRSRSDSHEADSTVFQCDPGYALQGS 1426
1180 AECVLEIENEFWOPSPPTCIAPCGGDLTGSPGVIISPNVPEPPPEKEDMWYVTSPP 1239
1427 AKITCVQANRFFQOPDPPTCIACGGNLTGPAGVIISPNVPEPPPEKEDMWYVTSPP 1486
1240 VYIALVNIENLEBEGYDFLHIYDGRDLSPLIGSFYQSOLPGRTESSNSLFLAFRSDAS 1299
1487 FVIALIFKSPMEBSYDFLHIYEBEDSNSPLIGYQSQARERLESSNSLFLAFRSDAS 1546
1300 VSANGFVIDYENRESCEFDGSIKNGTRVGSDLKGSVTTYCHGIEVEGISTLCIL 1359
1547 VGLSGFAIEFKERREACFDPGNIMNGTRVGTIDFKLSTIYQCDGKILDPSSITCVI 1606
1360 GPDGKPMWNNRPVCTAPCGGQYVSGDGVLSPNVPOYVTSQJCLYEVTVPKDYVWFGQ 1419
1607 GADKPSHDVLPSCNAPCGQYVSGEVLSPNPHNYTAGQICLYSITVPKSFVFGQ 1666
1420 FAFPHALNDVNEVHDGSHQSRLLSSLSGSHTEGSLPLATSNQVLKFSKAGLAPARGF 1479
1667 FAYFQTLNDLAEIJDGTHAQARLLSSLSGSHTEGSLPLATSNQVLKFSKAGLAPARGF 1726
1480 HFYQVAVPRTSATCCSVPEPRYGRKLGSDPSVGLIYREECNSGVALQSEPIICLPVPG 1539
1727 HFVQVAVPRTSDTCCSVPEPRYGRKLGSDPSVGLIYREECNSGVALQSEPIICLPVPG 1786
1540 ALAOMNAPTCVPCGCGNLTERGTLISPGFPEPYNSLNCWIKIYVBEAGIOIYVS 1539
1787 ALAOMNAPTCVPCGCGNLTERGTLISPGFPEPYNSLNCWIKIYVBEAGIOIYVS 1846
1600 FVTEBONDSLEVPDADNTVTMLGSFSGTVPALLNSTNQLYHFIYSDISVSAGFHE 1659
1447 FATEQNDSDLEIHDGDTAPRLGSFSGTVPALLNSTNQLYHFIYSDISVSAGFHE 1906
1660 YKTYGLSSCPREPAVPSNGVKTGERLYLVNDVVSFOCEPGYALQSHAHISCMFGYVRNYP 1719
1907 YKTYGLAACORPALPSNSIKIGDRYVNDVVSFOCEPGYALQSHAHISCMFGYVRNYP 1966
1720 PPLCIACCGTVEBEGVILSPGPGNVPNSMDCSKIALFVGRGHIQELNFTSTERNHD 1779
1967 SPLCIACCGTVEBEGVILSPGPGNVPNSMDCSKIALFVGRGHIQELNFTSTERNHD 2026
1780 YIEIRNGPYETSRMNGRFSGSELSLSTSHETTVYFHSQNSQNRPGFKLEYQAYELOE 1839
2027 FLEIQNGPYHNSPMIGQSGSTDLRALSLSTHETTVYFHSQNSQNRPGFKLEYQAYELOE 2086
1840 CPDPEPPANGIVRAGVNGVSTPECLPGYQTLGHPVLTGCHGTNRNMDHPLKCEVPC 1899
2087 CPDPEPPONGYVMSIDVSGVSFECPYGLIGHPVLTGCHGTNRNMDHPLKCEVPC 2146
1900 GGNITSSNGTYVSGFSPSSQDCWLVLPVIGHGVRMLSLIQEPSPDFTINDGP 1959
2147 GYNTSSQNGTYVSGFSPSSQDCWLVLPVIGHGVRMLSLIQEPSPDFTINDGP 2206
1960 QQTAPRLGVFTSRNAKKTVOGSSNOVLKFRDADATGIFAIASAY-----PLTK----- 2010
2207 DQNSPOLGVFTSRNAKKTVOGSSNOVLKFRDADATGIFAIASAY-----PLTK----- 2266
2011 -----CPP-----TILPNAEVTEN 2026
2267 WCLIQCCPTPCFOLKFLDSAGVYDS 2292

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RESULT 10
 US-10-276-934-11
 ; Sequence 11, Application US/10276934
 ; Publication No. US20030180750A1
 ; GENERAL INFORMATION:

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APPLICANT: University of Leeds
APPLICANT: Markham, Alexander F.
APPLICANT: Jackson, Andrew P.
APPLICANT: Woods, Christopher G.
TITLE OF INVENTION: Treatment of Cancer and Neurological Diseases
FILE REFERENCE: 9052-144
CURRENT APPLICATION NUMBER: US/10/276,934
PRIOR FILING DATE: 2002-11-20
PRIOR APPLICATION NUMBER: PCT/GB01/02240
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: GB0012186.3
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 2008
TYPE: PRT
ORGANISM: Homo sapiens
US-10-276-934-11

Query Match 44.6%; Score 7568.5; DB 14; Length 2008;
Best Local Similarity 66.7%; Pred. No. 0;
Matches 1328; Conservative 285; Mismatches 316; Indels 63; Gaps 8;

62 LTQVVGQGNMCPDPGIPERGRKLGSDFRGSSVQFTCNEGYDLOGSKRITCKVSDMF 121
39 VSQGVVALVSDMCDPDPGIPERGRKLGSDFRGSSVQFTCNEGYDLOGSKRITCKVSDMF 98
122 AAMSDHPRVCRARMCDAHLRPGSITSPNFIQYDNNAHCWIIITLANSKVIKLAEE 181
99 AAMSDHPRICRARCNSNLRGSGVITSPNFIQYDNNAHCWIIITLANSKVIKLAEE 158
182 FDLERGVDTLVGEGGDDGQKTYLVMSQNACSHPTPSRIE---SNSGDITWRQKT 238
159 FELERGVDTLVGAGVGDTRSVLYV-----LTSSVVDLTVSMNSQMLH--- 205
239 VLEICRDISSDARSQSVRSKPTSNVAVLPAPG-----TEIQQSGCDPPIPAYGRREG 293
206 -----LQSDS-----IGSPFKAVYQIEIKGGCGDPIPIYGRKTG 242
294 SRFHGDTLKECPAPAEIVGOKAITQKNNQMSAKKPGCVFSCFNFPSBQVVLSPNY 353
243 SSFLAGDTLFECPAEIVGOKAITQKNNQMSAKKPGCVFSCFNFPSBQVVLSPNY 302
354 PEDYGNLHLCWILLAPBSRIRHLAFNDIDYVPPDPLVIKQATAPLVLGTSSGNLP 413
303 PEEYGNMNCWMLIISPSGRIRHLAFNDIDYVPPDPLVIKQATAPLVLGTSSGNLP 362
414 SSITSGHVARLEQTOHSTGKGFNTFTTFRNECPDPGVPNGKRGFGSLQGSIS 473
363 SOLASSGHIVRLEQTOHSTGKGFNTFTTFRNECPDPGVPNGKRGFGSLQGSIS 422
474 FLCDGFLGTQGETITCVLKEGSVWNSAVLRCEAPCGGHLTSPSGTILSPGMPGYKD 533
423 FHODDFVKTQGSISITCIIQDGNVWVSITPREACCGHILTMSGVILPQMPGYKD 482
534 ALSCAWITEOPGYPIKITDRFKTEVNYDTLEVRDCKRTYASPLIGYHGTQVQFLIST 593
483 SLHCWITEOPGYPIKITDRFKTEVNYDTLEVRDCKRTYASPLIGYHGTQVQFLIST 542
594 SNVYLLFSTDKSHSDIGPOLRYETITLQSDHCDPPIPVNGQHGNDPFGVALVTPSCD 653
543 GNFYLLFSTDKSHSDIGPOLRYETITLQSDHCDPPIPVNGQHGNDPFGVALVTPSCD 602
654 SGYTLSDGEPLECEPNFQWGRALPSCALCGFIQGSSTGTLISGFPDPFYNNLNCWTMI 713
603 PGYTLSDDEPLVGRNRNQMHALPSCDALCGGYIQGSSTGTLISGFPDPFYNNLNCWTMI 662
714 ETSHGKGVFTFTFTHLESCHDYLITENSGFTFOPLKQLTGSRLPAISGLKGNFTAOV 773
663 EVSHGKGVQMIFFTHLESCHDYLITENSGFTFOPLKQLTGSRLPAISGLKGNFTAOV 722
774 RFLSDPMSYEGFNITPSEYDLCEPCEPVPAYSIRKGLQFGVGDVTLTFSGFPYRLBGT 833

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Db	723	RFTSDBSITSEGENITTSSEYDLEBCDDPGVAPASRRRI	GFHFVGSDLSLTSCELGRLBGA	782
Qy	834	ARITCLGRRRLWSSPLPRCVAECGNSVTGTCOTLLS	PNEPVVNNNHHCISYSIQOPK	893
Db	783	TKLTUCGGGRRVWASAPLRCAECGASVKNEGTLLS	PNPNSYDNHHCITKIEFEAK	842
Qy	894	GJLQKAPRLESBDVUKYVDGNNSARLLGVSHSEMMGV	TLNSTRSSLLDFTTDAEN	953
Db	843	GJHURRSFOLFEGBDYLLKYDGOSSSRPLGFTYKNE	LLGLTLNSTRSSNLMLEFNTNGD	902
Qy	954	TSKGELHFSFELIKCEDPGTKFGKYVDEHFAFGSS	VSESCDCEYSLRSEELTCLS	1011
Db	903	TDGQFOLTYSFDLVKCEDPGIEVNGYRIRDESH	FDYDVLVYSCNPGYAMHSNTLLCS	962
Qy	1014	GERRTMDRPLPTVAAACGGTVKGEVSGOVLSPGY	PAPYBHNLNCTWTLBAEGCTTGLHF	1073
Db	963	GDRRWMDKPLPSCIACCGQIHAATYSGRILSPGY	PAPYNNHCTWILTEADGKITSLHF	1022
Qy	1074	LYEDTEEVADVLRIMDPVESGVLLKELSGPAL	PKDHSFMSVNLQSTDEFTSKOBA	1133
Db	1023	IYDTEMAHDILKVMGVPDSDLLKEMSGALPEDI	HSFTNSLTITQEPDSDFIKSGHS	1082
Qy	1134	IQPSVSTARSNDPGI.PONGSRSGDSWEAGDSTV	POCDPGVALQGSAAETSCYKLENREPW	1193
Db	1083	IOFSTSIATCNDPGMPONGTRYGDSREAGDVT	POCDPGYOLQOQAKITCYQVNNRPFM	1142
Qy	1194	QESPFPICAPCGGDLTGPBGVLLSPVYPPY	PGKCBMKVYSPDVTALAVENFLEP	1253
Db	1143	QDPDPICIAACGNLTGPAGVLLSPYPPY	PGKCBMDRVANDEPYALIFPSFNER	1202
Qy	1254	GYDFLHTYGRDLSPLISFPYGSOLPGRI	IESSNSLFLAFRSDASVSNAGVVDYENP	1313
Db	1203	SYDFLHTYGEBSNSPLISYOGSOQAPERI	IESGNSLFLAFRSDASVGLSGALIEFKKP	1262
Qy	1314	RESCFPGSIKNGTRGSDYLKIGSSVTYCHGVE	EGSTLSCILGSDGKPMWNNRPV	1373
Db	1263	REACDPRGUMNGTRVGDYFKLGSTITTY	QDSGYKILDPSSITTYIGADGKPSMDVULPS	1322
Qy	1374	CTAPCGGQYVSGDGVVLSPBNYPONTSGO	ILCYFVTPKDYVVFQGFAPFTALNDVYEV	1433
Db	1323	CNAPCGGQYVTSSEGVVLSPBNYPHNTAG	QICLXSTIVPEKVFQGFAPFTALNDLAEI	1382
Qy	1434	HGHSGHSLLSLSGSHGESLPLATSNQVLI	KXSAGLAPARGFHHVYQAVPRTSATQ	1493
Db	1383	FGHTAQAARLLSSLSGSHGESLPLATSNQVLI	LRFSASGSARGFHHVYQAVVRTSDTQ	1442
Qy	1494	CSSVEPRYKRLGSDFSVGAIVRECNCSGVAL	QOSPEIECLPYGALAAQNNVAPICVY	1553
Db	1443	CSSVEPRYGRRIIGSEFSAGSIIVRECNPG	YLLQSTALHCOQSPNMAQNNDTIPBCVY	1502
Qy	1554	POCGULTERRGILLSPGFPEPYLANLNCV	KIIVPEAGIOTIOVSPVTEQNMDSLEVD	1613
Db	1503	POSGFPTORRGITLSPGYPEPYGNLNCIM	KIIVYEGSGIOTIOVISAFTEQNMDSLEIHD	1562
Qy	1614	GADNTVTMIGSFGTTVPALLNSTNSQVLY	LHFYSPDISVSAGFPLEKXTVGLSCSREPAV	1673
Db	1563	GQDVTAPRLGSGTTPALLNSTNSQVLYLH	FOGDISVLAAGFPLEKXTVGLAQCQEPAL	1622
Qy	1674	PSNGVKTERTLVNDVYSFOCEPGYALOG	HANHISCMPTVARNMYPPPLCIAOQGTVEE	1733
Db	1623	PSNISKIGDRYVNDVYSFOCEPGYTLQGR	SHISCMPTVARNMYPPPLCIATGCGTJST	1682
Qy	1734	MEGVILSGFPGNYPNSNMDGSMKIALP	YGFAGHIQFINFSEPHNDIELRNOPYEFSRM	1793
Db	1683	LGCVILSGFPGFSPYNNLDCWTKRISL	PGYAHAIQFINFSTEANHDLELQNGGYHSPM	1742
Qy	1794	MGRPBGSELPSLLSTSHETTVYFVSHDS	QNRPGFKLEYQAYLEQCEPDEPFANGIVRG	1853
Db	1743	IGQFSGTDLPALLSTHETTLIHFYSDHS	QNRQFKLAYQAYLELQCPDPPEPQNGYMIN	1802
Qy	1854	AGVNVGQVTEPCLPGVOLTGHPVLTQ	OHGNNRWMDPLKCEVPCCGANTSSNGYVYSP	1913

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Db      1803 SDYVGQSVSECEYGYLLIGHPVLTQCHGINRMNMPFPCRDAPCGYNTVSQNGTIYSP 1862
QY      1914 GPPSYSSSOOCWMLITPPIGHGRNLMSLQTEPSSDFTIMDGPOTAPRLGVFRSM 1973
Db      1863 GPFDEYPLKACIMLITVPSPGHVINTFLTQTEVANDVYLAWMDGPQNSPOLGVFSGNT 1922
QY      1974 AKTIQSSSNVOLLKFRHDAATGGIFAIAFSAY----PLTK-----CPP----- 2014
Db      1923 ALETYASTNQVLLKFHSHDFENGCFVLIYNFHGULFTPLVKTENSMWCLIQCCPTPEFOL 1982
QY      2015 TILPAAHYTEN 2026
Db      1983 KFLDSABGVDS 1994

RESULT 11
US-10-276-934-9
; Sequence 9, Application US/10276934
; Publication No. US20030180750A1
; GENERAL INFORMATION:
; APPLICANT: University of Leeds
; APPLICANT: Markham, Alexander F.
; APPLICANT: Jackson, Andrew P.
; APPLICANT: Woods, Christopher G.
; TITLE OF INVENTION: Treatment of Cancer and Neurological Diseases
; FILE REFERENCE: 9052-144
; CURRENT APPLICATION NUMBER: US/10/276,934
; CURRENT FILING DATE: 2002-11-20
; PRIOR APPLICATION NUMBER: PCT/GB01/02240
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: GB0012186.3
; PRIOR FILING DATE: 2000-05-20
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 1826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-934-9

Query Match      41.8%; Score 7098; DB 14; Length 1826;
Best Local Similarity 68.1%; Pted. No. 0;
Matches 1241; Conservative 262; Mismatches 276; Indels 44; Gaps 5;

QY      62 LTVGVVSGQHNMPPDPCGIEPERGRLGSDPRLGSSVOFTNCEGYDIOGSKRITCMKVSMF 121
Db      39 VSGQGVALVSDMCPDPCGIEPENGRRAGSDPRVAGANVOFSGEDNYVTLQSSKSTICQRTETL 98
QY      122 AANSDRPVCRAAMCAHLRGSGIITSNPNFIQYDNNACWMIITALNPSKYIKLAE 181
Db      99 AANSDRPFCRAATCCSNLRGSGVITSNPNVQYEDNACWMIITTPDPKVIKLA 158
QY      182 FDLERGGDTLVYVGDGDODDOKTIVLYMSQNASDSBPHRPGRIPE---SMGSDIRQOKT 238
Db      159 FELERGGDTLVYGDAGKVDTRSLVY-----LTGSSVPLIYMSNQMWLH-- 205
QY      239 VLEICRDISSDARSQSVKRSKPTSNANVELVAPG-----TEIEQSGCGDPGIPAYGRREG 293
Db      206 -----LQSDS-----IGSPGKAVYQIEIKEGCGDPIGIPAYGKRTG 242
QY      294 SRPHHGDTLKFGCPAPFELVQKATTCQKQNNQMSAKKGCVPFSCFNFTTSFSGVVLSTPNY 353
Db      243 SSTLHGDTLTFECPAPFELVGERVLTTCQNNQMSGNKKSQVSCFNFPTASSGIITLSPNY 302
QY      354 PEDYGNHLHCWMLILARPESRTHLAFNDIDVEPODFPVIKDGATAEAPVLTGFSGNQLP 413
Db      303 PEYGNMNCWMLIISEPESRTHLAFNDIDVEPODFPVLAVKDDGISTITVLTGFSGNVEP 362
QY      414 SSTTSGHVALEFQDTHSTGKRGVNTFTFRHNECPDGPVNVNKKRFGSLSLGSSIS 473
Db      363 SOLASSGHVLRLEFQSDHSTTGRGNFTVYTFGQNECHADPGIPINGRFRFGDRFLGSSVS 422
QY      474 FLCDRFLGTQSGSEFTITCVLKEGSAVNMASVLRCAAPCGGHLTSPSGITLSPGMGPFKD 513

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423 FHDDDFVKTQSGESITCICDGNVWSSVTPRCAPCGSHLASSGVILPWPMPGYDD 482
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1623 PENVGTGERVLYNDVVSFQCEPGVYALOGHAHISCMPTGRWBNYPPPLIAOCCGTVEE 1682
1623 PENVGTGERVLYNDVVSFQCEPGVYALOGHAHISCMPTGRWBNYPPPLIAOCCGTVEE 1682
1734 MEGVILSPGPPGPNYPSNDCSMKIALPVGFAHIOPLNSTEPNDHDIIRNGPYTSSM 1793
1734 MEGVILSPGPPGPNYPSNDCSMKIALPVGFAHIOPLNSTEPNDHDIIRNGPYTSSM 1793
1683 IGVILSPGPPGPNYPSNDCSMKIALPVGFAHIOPLNSTEPNDHDIIRNGPYTSSM 1742
1683 IGVILSPGPPGPNYPSNDCSMKIALPVGFAHIOPLNSTEPNDHDIIRNGPYTSSM 1742
1794 MGRFSGELPSLSLSTSHETTYVYFSDHSONRPGFLXEOVLEOCBDEPPEPANGIYVG 1853
1794 MGRFSGELPSLSLSTSHETTYVYFSDHSONRPGFLXEOVLEOCBDEPPEPANGIYVG 1853
1743 IGVILSPGPPGPNYPSNDCSMKIALPVGFAHIOPLNSTEPNDHDIIRNGPYTSSM 1802
1743 IGVILSPGPPGPNYPSNDCSMKIALPVGFAHIOPLNSTEPNDHDIIRNGPYTSSM 1802
1854 AGYVNGSVTFECLPGYQLTGHP 1876
1854 AGYVNGSVTFECLPGYQLTGHP 1876
1803 SDYVNGSVTFECLPGYQLTGHP 1825
1803 SDYVNGSVTFECLPGYQLTGHP 1825

RESULT 12
US-10-276-934-10
; Sequence 10, Application US/10276934
; Publication No. US20030180750A1
; APPLICANT: Markham, Alexander F.
; APPLICANT: Jackson, Andrew P.
; APPLICANT: Woods, Christopher G.
; TITLE OF INVENTION: Treatment of Cancer and Neurological Diseases
; FILE REFERENCE: 9052-144
; CURRENT APPLICATION NUMBER: US/10/276,934
; CURRENT FILING DATE: 2002-11-20
; PRIOR APPLICATION NUMBER: PCT/GB01/02240
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: GB0012186.3
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 1800
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-934-10

Query Match 40.9%; Score 6949; DB 14; Length 1800;
Best Local Similarity 67.9%; Pred. No. 0;
Matches 1216; Conservative 259; Mismatches 272; Indels 44; Gaps 5;

62 LTVGVSGCHNMCPDPIBERGKRLGSDPRLGSSVQFTCNEGYDLOGSKRITCMKYSDMF 121
62 LTVGVSGCHNMCPDPIBERGKRLGSDPRLGSSVQFTCNEGYDLOGSKRITCMKYSDMF 121
39 VSGGVYALVSDKCPDPIBERGKRLGSDPRLGSSVQFTCNEGYDLOGSKRITCMKYSDMF 98
39 VSGGVYALVSDKCPDPIBERGKRLGSDPRLGSSVQFTCNEGYDLOGSKRITCMKYSDMF 98
122 AAWSDHRCVACRAMCAHLRSGEITTSNPIQYNNNAHCWITIALNPSKIYKIAFAEF 181
122 AAWSDHRCVACRAMCAHLRSGEITTSNPIQYNNNAHCWITIALNPSKIYKIAFAEF 181
99 AAWSDHRCVACRAMCAHLRSGEITTSNPIQYNNNAHCWITIALNPSKIYKIAFAEF 158
99 AAWSDHRCVACRAMCAHLRSGEITTSNPIQYNNNAHCWITIALNPSKIYKIAFAEF 158
182 FDLERGVDTLTVGDGODGODQKTVLYMSQACSDSHHTGSRPE---SWSGDIWPKQMT 238
182 FDLERGVDTLTVGDGODGODQKTVLYMSQACSDSHHTGSRPE---SWSGDIWPKQMT 238
159 FELERGVDTLTVGDGODGODQKTVLYMSQACSDSHHTGSRPE---SWSGDIWPKQMT 205
159 FELERGVDTLTVGDGODGODQKTVLYMSQACSDSHHTGSRPE---SWSGDIWPKQMT 205
239 VLEICRDISSDARSRSVRSKPTSNVAVELVABG-----TELEQSGCSDPGIPAYGRREG 293
239 VLEICRDISSDARSRSVRSKPTSNVAVELVABG-----TELEQSGCSDPGIPAYGRREG 293
206 -----LQSDDS-----IGSGFPAVVGELIKGCGDGPDIAYGRREG 242
206 -----LQSDDS-----IGSGFPAVVGELIKGCGDGPDIAYGRREG 242
294 SRFHGDDTLKEFCQAPAFELVQCAITCOXNNQMSAKKPGCVSPCFNFTSPSGVILSPNY 353
294 SRFHGDDTLKEFCQAPAFELVQCAITCOXNNQMSAKKPGCVSPCFNFTSPSGVILSPNY 353
243 SSFLHGDITLFECPAPAFELVQCAITCOXNNQMSAKKPGCVSPCFNFTSPSGVILSPNY 302
243 SSFLHGDITLFECPAPAFELVQCAITCOXNNQMSAKKPGCVSPCFNFTSPSGVILSPNY 302
354 PEDYGNHLHCWMLIARPESRHLAFNDIDVEPQPFVLYKQDATLAPVLTGTFSGNQLP 413
354 PEDYGNHLHCWMLIARPESRHLAFNDIDVEPQPFVLYKQDATLAPVLTGTFSGNQLP 413

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Db 303 PEEVGNMNCWMLILSPGSRHILFENDFVPEQDFLAVKDDGISDITVLGTFSGNEVP 362
Qy 414 SSTSSGHVAREFQDTHSTGKGFNTFTTFPHNEPDPGVNKGKREDSIQLGSSIS 473
Db 363 SOLASSSHVAREFQDTHSTGKGFNTFTTFPHNEPDPGVNKGKREDSIQLGSSIS 422
Qy 474 FLDEGEFLTGSEETICVLEKESGVNNSAVLRCAPCGHLLTSPSGTILSPMPGPKYK 533
Db 423 FHDDGVKVTQGESSEITCIIQDGNVWMSVTPRCAPCGHLLTSPSGTILSPMPGPKYK 482
Qy 534 ALSCAWIEAOPGYPIKITFDREKTEVNYDTLEVRDRTYSADLLGVNHTQVQPLIST 593
Db 483 SLHCWEIIEAKPGHSIKITFDREKTEVNYDTLEVRDRTYSADLLGVNHTQVQPLIST 542
Qy 594 SNLYLLFSTDKSHSDIGFOLARETTLQSDHCLDPCIPVNGRQNDPVGALYTFSCD 653
Db 543 GNMWYLLFTYDNRSSISGLIHYESVLTESDCLDPCIPVNGRQNDPVGALYTFSCD 602
Qy 654 SGYTLSDGEPLCEPNEFQWMSRALPSCBLCGCFIQCSSGTILSPGPDFFYNNINACTWIT 713
Db 603 PGYTLSDDEPLVERNRHQMWHALPSCDALCGYIQCSSGTIVLSPGPDFFYNNINACTWIT 662
Qy 714 EYSHGKGVFTFTFPHLESGLDYLITENGSTFQPLRQLTGSRLPAPISAGLVNFTAOY 773
Db 663 EVSHGKGVQWIFFTPHLESGLDYLITENGSTFQPLRQLTGSRLPAPISAGLVNFTAOY 722
Qy 774 RFLSDSMSVEGNITFSEYDLPECEPVPAYSIKGLQFQGDILTFCSPGYRLGCT 833
Db 723 RFLSDSMSVEGNITFSEYDLPECEPVPAYSIKGLQFQGDILTFCSPGYRLGCT 782
Qy 834 ARITLCGRRRLWSSPLPRCAECGNSVTGCTGLSPNFPVYNNNNHECTIYSIQTOPCK 893
Db 783 TKLTLCGGRRVMSAPLRCAECGNSVTGCTGLSPNFPVYNNNNHECTIYSIQTOPCK 842
Qy 894 GLOLKARAFELSGDYLVKTDGNNNSARLLGVSHBANGVTILNSTRSSIMLDFITDAEN 953
Db 843 GHILRTSRFOLFEGDYLKYVDGSSSRPGLTKEHLLILNSTRSSIMLDFITDAEN 902
Qy 954 TSXGFLHFSFELIKCEDPGTPEKFGKYHDEGHFPASSVSFCSDGYLSRGSEELICIS 1013
Db 903 TDGQFQTLTYSFPLVCKEDPGIAPNYGRIKDBGHFTDVTVALVSCNGYAHGSSNLTLCIS 962
Qy 1014 GERRITDRPLPTCAECGTVRGEVSGVLSPGYPAPYEHNLNCTITIEAAGCTIGLHF 1073
Db 963 GERRITDRPLPTCAECGTVRGEVSGVLSPGYPAPYEHNLNCTITIEAAGCTIGLHF 1022
Qy 1074 LVPTDEVDVLRINQGVESGVLLKELSGPALPKDLHSTFNSVULQFSTDFTSKQGA 1133
Db 1023 IVDTEMAHDILKVMQGPVDSILLKEMSGSALPBDIHSFNSLTLQFSDFFISKSGFS 1082
Qy 1134 IOPSVTATSCNDPGIPONGSRGSDMEAGDSVTFQCCDGYALQGSABISCVIENRPFM 1193
Db 1083 IOPSVTATSCNDPGIPONGSRGSDMEAGDSVTFQCCDGYALQGSABISCVIENRPFM 1142
Qy 1194 QPSPPTCIAPCGGDLTPSGSVILSPNYPEBPYKXCDMKVTVSPDYVALVENIENLEP 1253
Db 1143 QPSPPTCIAPCGGDLTPSGSVILSPNYPEBPYKXCDMKVTVSPDYVALVENIENLEP 1202
Qy 1254 GYDFLHITVGRDLSPLIGSFYGSQPLGRLESSNSLFLAFRSDASVSNAGFYIDYENP 1313
Db 1203 SYDFLHITVGRDLSPLIGSFYGSQPLGRLESSNSLFLAFRSDASVSNAGFYIDYENP 1262
Qy 1314 RESCPGSIKNGTRVGSDDLKLGSSVTVYCHGVEYEGTSLSCILGPGKXPMNNPRV 1373
Db 1263 RESCPGSIKNGTRVGSDDLKLGSSVTVYCHGVEYEGTSLSCILGPGKXPMNNPRV 1322
Qy 1374 CTAPCGQYVSGDVVLSPNYPQNTYSGQICLYFVTVPKDYVVFQGFAPHTALNDVVEY 1433
Db 1323 CTAPCGQYVSGDVVLSPNYPQNTYSGQICLYFVTVPKDYVVFQGFAPHTALNDVVEY 1382
Qy 1434 HGHSHSLSSLSHSGESLPLATSNQVLIKESAKGLAPRGHFTYQAVPRTSATQ 1493
Db 1382 HGHSHSLSSLSHSGESLPLATSNQVLIKESAKGLAPRGHFTYQAVPRTSATQ 1442

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Db 1383 PDGTHAQBALLSSLSGSHGETLPLATSNQVLIKESAKGLAPRGHFTYQAVPRTSATQ 1442
Qy 1494 CSSVPEPRYGRKLGSDFSVGAIVRECNNGVYALQSSPELECLPVPALQOMVNSACTV 1553
Db 1443 CSSVPEPRYGRKLGSDFSVGAIVRECNNGVYALQSSPELECLPVPALQOMVNSACTV 1502
Qy 1554 PCGMLTERRGITLSPGPEPYLNSLNCWKIVVEGAGIQIQVSVFVEQNMWDSLEVP 1613
Db 1503 PCGMLTERRGITLSPGPEPYLNSLNCWKIVVEGAGIQIQVSVFVEQNMWDSLEVP 1562
Qy 1614 GADNVTMLGSGFTVPALNLSNOLYLFHYSOISVSAGFPHLEKTVGLSSCEPVP 1673
Db 1563 GADNVTMLGSGFTVPALNLSNOLYLFHYSOISVSAGFPHLEKTVGLSSCEPVP 1622
Qy 1674 PSNGVTKGGRVYNVVSFQCEPGVYALQGHASICMPGVWRWNPPLICIAQCCTVYE 1733
Db 1623 PSNGVTKGGRVYNVVSFQCEPGVYALQGHASICMPGVWRWNPPLICIAQCCTVYE 1682
Qy 1734 MEGVILSPGPNYPSNMDCSWKIALPVGFAHIOFLNSTEPNHDYIEIRNGPYETSHM 1793
Db 1683 MEGVILSPGPNYPSNMDCSWKIALPVGFAHIOFLNSTEPNHDYIEIRNGPYETSHM 1742
Qy 1794 MGRFGSELPSLSLSTSHETTVYFHSQSNQNPGRKLEYQAYELCEPDPE 1844
Db 1743 MGRFGSELPSLSLSTSHETTVYFHSQSNQNPGRKLEYQAYELCEPDPE 1793

RESULT 13
US-10-276-934-12
; Sequence 12, Application US/10276934
; Publication No. US20030180750A1
; GENERAL INFORMATION:
; APPLICANT: University of Leeds
; APPLICANT: Marham, Alexander F.
; APPLICANT: Jackson, Andrew P.
; APPLICANT: Woods, Christopher G.
; TITLE OF INVENTION: Treatment of Cancer and Neurological Diseases
; FILE REFERENCE: 9052-144
; CURRENT APPLICATION NUMBER: US/10/276,934
; PRIOR FILING DATE: 2002-11-20
; PRIOR APPLICATION NUMBER: PCT/GB01/02240
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: GB0012186.3
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 1783
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-934-12

Query Match 40.8%; Score 6936; DB 14; Length 1783;
Best Local Similarity 68.1%; Pred. No. 0;
Matches 1213; Conservative 258; Mismatches 266; Indels 44; Gaps 5;

Qy 62 LTVQVSGCHNCCPPIPERGKRLGSDPRLGSSVQFQCNBEGYDQSGKRITCMKYSDF 121
Db 39 VSQGVVALVDMCPPIPERGKRLGSDPRLGSSVQFQCNBEGYDQSGKRITCMKYSDF 98
Qy 122 AAMDHRPVCRAKMDAHLRGPSSGITSPPNPIQYDNNNAHCWITITALNPSKVILAEFE 181
Db 99 AAMDHRPVCRAKMDAHLRGPSSGITSPPNPIQYDNNNAHCWITITALNPSKVILAEFE 158
Qy 182 FDLERGYDTLLVYGGGQDQKTVLYMQNACSDSEPHTPGSRIFP---SMGDIYRQKVT 238
Db 159 FELERGYDTLLVYGGGQDQKTVLYMQNACSDSEPHTPGSRIFP---SMGDIYRQKVT 205
Qy 239 VLEICRDISSSARAGSRKSPKTSNAVELVAPG---TEIEQSCGDPGIPAYGREG 293
Db 206 -----LQSDS-----IGSPGKAVYQIEIKGCGDPGIPAYGKRTG 242
Qy 294 SRFHNDTLKRECQAPFELVQKAITCQKNNQWMAKKGCVFSFNFSTPSGVLVSPVY 353
Db 242 SRFHNDTLKRECQAPFELVQKAITCQKNNQWMAKKGCVFSFNFSTPSGVLVSPVY 209

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Db 243 SSFLHGGTLTFECRAAEIVGERVITCOQNNOMSKNRCVSCFSGFFFTASSGIILSPNY 302
Qy 354 PEDIYGNHLCVWMLIARPEBRIHLAFNDIDIVEPOFDFVIKDGATAEAPVLTGFSGNOLP 413
Db 303 PEEYGNMNCVMWLIISPEGRIRHLIFNDPVEPOFDELAVIDDOIISDIIVLTGTFSSGNEVP 362
Qy 414 SSTSSGHVAREFQDHDSTGKRGFNITFTFRNNECPDPVPMNGRPFDDSLDGLSSIS 473
Db 363 SQAASSGHIVLEBQSDHSTTGKGFNITFTFGNBECHDPGIPINGRRPDRFLGSSVS 422
Qy 474 FLDEGELTQOGETTICVLEKESGVWNSAVLRCEAPCGHLTSPSGTILSPGMPGYKD 533
Db 423 FHDDGKVTQGSSESIICILQDGNVWMSVIVPREACGHLTASSVILPFGMPGYKD 482
Qy 534 ALSCAWVIEAOPGYPIKITFDREKTEVNYDTLEVDRGRTVSAPLIGVHGTQVPOFLIST 593
Db 483 SLHCEWIIIAKPGHSIKITFDREKTEVNYDTLEVDRGRTVSAPLIGVHGTQVPOFLIST 542
Qy 594 SNLYLILFSTDKSHSDIGFOLARVETITLOSCHLDPITPNVGNHNDPFGALVYFSSCD 653
Db 543 GNMVYLFTTNDSSSIFLIHESVTLSDSCLDPEI PVNGHHGDFGIRSTVTFSCD 602
Qy 654 SGYTLSDGEPLCEGPNFQMSRALPSCBALCGGFQGSSTILSPGPFDPYNNLNCWII 713
Db 603 PGYTLSDDEPLVCERNQMHALPSCDALCGGYIQGSGTVLSGPFDFPNSLNCWTI 662
Qy 714 ETSHGKGVFTFHTFHLESCHDYLITENGSTFOTPLQTLGSRLPADISAGLYGNFTAOV 773
Db 663 EVSHGKGVQMI FHTFHLESCHDYLITENGSTFSEPPVRLTGSVLPHTIKALGKGNFTAOV 722
Qy 774 RFTSDPMSYEGFNITSEYDLRECEBEVPAYVIRKGLQPGVODTLTSCFCGYRLGCT 833
Db 723 RFTSDPMSYEGFNITSEYDLRECEBEVPAYVIRKGLQPGVODTLTSCFCGYRLGCT 782
Qy 834 ARTTLCGRRRLWSSPLPRCAVECGNVTQGTLLSPNPNVNNNNHECTIYSIQTOPK 893
Db 783 TXLTLCGGRWVASAPRCAVECGNVTQGTLLSPNPNVNNNNHECTIYSIQTOPK 842
Qy 894 GIOLKARAFELSGDVLKVTGDNNSNARLLGVPSHSEMKVTLNSTSSLMDLFTIDAEN 953
Db 843 GIHLRTSFOLEPBDTLKVDGKSSSRPLGTFPKNELLLIINSTNHLLEPNTGSD 902
Qy 954 TSKGFLHFSFELIKEDRGTPKFGYKXNDGEGFPASSVSFGCDPRYSLRGSEELLCLS 1013
Db 903 TDGSPOLTYTSFPLVKCEDPGIPIYGYRIRDEGFTDTVVLVYSCNPEYAMHGSJTLTCLS 962
Qy 1014 GERRTMDRPLPTCAVACCGTVRGEVSGOVLSPGYAPAEHNLNCIWTIEAAGCTTGLH 1073
Db 963 GDRRWMDKPLPSCIAECCGOIHAATSGRIISPGYAPAEHNLNCIWTIEAAGCTTGLH 1022
Qy 1074 LVFDTEBHDVLRIMDGPVSEGVLLKELSGPALPKDLASTFNSVVLQFSDFTSKOGFA 1133
Db 1023 IVEDEMAHDILKVMDDPVDSDILKEMSGSALPEDIHSTFNSLTLQFSDDFISKSGFS 1082
Qy 1134 IORSVSTATSCNBPGLFQNSRSGDSWEADSTVFQCDPRYALQSAEISCVKIEKRFEM 1193
Db 1083 IQESTSIATCNDPQMONGTRYGDSREADTYTFQCDPRYALQSAEISCVKIEKRFEM 1142
Qy 1194 QPSPPTCIACCGGLTGPSPGVLISPNYPEYPPKGEKCDMKVTVSPDVIALVFNIFLPE 1253
Db 1143 QPSPPTCIACCGGLTGPSPGVLISPNYPEYPPKGEKCDMKVTVSPDVIALVFNIFLPE 1202
Qy 1254 GYDFLHIYDGRDLSPLIGS FYGSQLPGRILESSNSLFLAFRSDASVSNAGFYDYTENP 1313
Db 1203 SYDFLHIYEGEDSNPLIGSYGQOABERIESSGNSLFLAFRSDASVSNAGFYDYTENP 1262
Qy 1314 RESCFDGGSIKNGRVSDDLKGSVYTYHGGIEVEGCTSLSSILGPDGKPMANNRPV 1373
Db 1263 REACFPDGNIMNGRVTDFRLGSGTITVYQDSDGKILIDPSSITCVIGADKPSMDOVLPS 1322
Qy 1374 CTAPCGGYGSDGVVSPVYPOVYTSQICLVFVTVPKYVVGQAFPHALNDVVEV 1433

Db 1323 CNAPEGQYTGSEGVVLSPNYPHNYTAGOICLYSITVPEKFEVVGQAFYOTALNDLAE 1382
Qy 1434 HDGHSORSLSSLSGSHGESIPLATSNVLIKESAKGLAPRGHFPVYQAVPRRSATO 1493
Db 1383 FDCGTHAQRSLSSLSGSHGESIPLATSNVLIKESAKGLAPRGHFPVYQAVPRRSATO 1442
Qy 1494 CSVPEPRYKGRIGSPVSAIVRPECNAGSYALQGSPEIECLVPGLAOMNYSAPICV 1553
Db 1443 CSVPEPRYKGRIGSPVSAIVRPECNAGSYALQGSPEIECLVPGLAOMNYSAPICV 1502
Qy 1554 PCGGLTERKRTILSPGPEPYLNSLNCWIKIIVPEAGAGIQTQVSPVTEQNMDSLEVP 1613
Db 1503 PCGGLTERKRTILSPGPEPYLNSLNCWIKIIVPEAGAGIQTQVSPVTEQNMDSLEVP 1562
Qy 1614 GADNVTYMLGSEGGTVPALLNSTSNQLYHFPISDSISVSAAGHLEKTYGLSSCEBPV 1673
Db 1563 GGVTAAPRLGSPFGTVPALLNSTSNQLYHFPISDSISVSAAGHLEKTYGLSSCEBPV 1622
Qy 1674 PSNGVATGERVYNDVVSFQCEBRYALQGHANISCMPTGRMRYNPPLCTIACCGVVEE 1733
Db 1623 PSNGVATGERVYNDVVSFQCEBRYALQGHANISCMPTGRMRYNPPLCTIACCGVVEE 1682
Qy 1734 MEGVILSPGPGNYPNSMDCSWKIALPVFGAHIOELNFTSEBNDYIEIRNGPYETSRM 1793
Db 1683 LGGVILSPGPGNYPNSMDCSWKIALPVFGAHIOELNFTSEBNDYIEIRNGPYETSRM 1742
Qy 1794 MGRFSGSELPSSLLSTSHETTVYFHSNDSQNRPGFLEYOA 1834
Db 1743 IGFSGGTDLPALALSTHETTLHFYSNDSQNRPGFLEYOA 1783

RESULT 14
US-10-016-248-49
; Sequence 49, Application US/10016248
; Publication No. US20040033491A1
; GENERAL INFORMATION:
; APPLICANT: Alebrook et al.
; TITLE OR INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-218
; CURRENT APPLICATION NUMBER: US/10/016, 248
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/254, 329
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/291, 037
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/255, 648
; PRIOR FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 60/297, 173
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: 60/309, 258
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/326, 393
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/315, 639
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 49
; LENGTH: 1048
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-016-248-49

Query Match 24.9%; Score 4226; DB 15; Length 1048;
Best Local Similarity 70.2%; Pred. No. 1,4e-293;
Matches 735; Conservative 153; Mismatches 159; Indels 0; Gaps 0;

Qy 718 GKGVFTFTHLESCHDYLITENGSTFOTPLQTLGSRLPADISAGLYGNFTAOVRFIS 777
Db 1 GKGVQMI FHTFHLESCHDYLITENGSTFSEPPVRLTGSVLPHTIKALGKGNFTAOVRFIS 60
Qy 778 DFMSEGFNITPSEVDLECEBEVPAYVIRKGLQPGVODTLTSCFCGYRLGCTARIT 837

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Db      61 DFEISYEGFNITESEYDLEPCDDPGVAFSRRIGPHFVGVDLSLFCPLGRLEGATKLT 120
Qy      838 CUGGRRLWSSPLPRCAECCGNSVTGCTGTLSPNPNVNNNHETIYSIQOPGKIOL 897
Db      121 CUGGGRWWSAPLRCAECCGASVKNNEGTLSPNPNVNNNHETIYKITEAGGHL 180
Qy      898 KARAFELSEEDVAKVYDGNNSARLLGVFSHSEMMGVTLNSTSSIMLDPITDAENTS 957
Db      181 KTRSFQLEEDTKYVDGKDSRRPLCTFTKMLGLILNSTNHLMEFNNGSTDDG 240
Qy      958 FELHFSFELIKCEDPQTPKFGYKVADEGHFAGSSVSFSCDPGYSLRGSEILLCLSGRR 1017
Db      241 FOLTYSFLDKCEDPGIPIVYGRIRDEGHFTDTVLVYSCNPGYAMHGSITLCLSGDRR 300
Qy      1018 TWRRLPTCAECCGTVRGEVSGOVLSPGPAVEHNNLCIWTIEAGCTTGLHVLVD 1077
Db      301 VMDKPLPSCIAECCGGGIIHAATSGRIISPGVAPYDNNHCTWIEADPGCTTSLHFIVD 360
Qy      1078 TEEDHVLRIWDPVSESVLLKELSGPALPKDLSHTFNSVVLQFTDFTSKOGFAIOPS 1137
Db      361 TEWAHDLKXWDPVDSDLILKEMSGALPEDIHSTFNSLTLOPDDFPIKSGFSIORS 420
Qy      1138 VSTATSCNDPEIPONGSRSGDSWEAGDSTVFQCDPGYALOGSAEISCVKIENRFWQSP 1197
Db      421 TSAATCNDPEMPQNGTRVYDGSREAGDTVTFQCDPGYALOGAKITCVQINNRFWQSP 480
Qy      1198 PTCIAACGGDLTPRSGVILSPNTPPEYPRGKEDMKVTVSPDVILVFNILFLEPGYD 1257
Db      481 PTCIAACGGDLTPAGVILSPNTPPEYPRGKEDMKVTVSPDVILVFNILFLEPGYD 540
Qy      1258 LHIYDGRDLSPLIGSFYGSQOLPGRIESSNSNLFILAFRSDASVSNAGVIDYTEMNRESC 1317
Db      541 LHIYBEGDMSPLIGSFYGSQOLPGRIESSNSNLFILAFRSDASVSNAGVIDYTEMNRESC 600
Qy      1318 FDFGSIKNGTRVSGDLKLGSSVTYCHGYVEGTSITLSCIAGDPKPVNNNRPVCTAP 1377
Db      601 FDFGSIKNGTRVSGDLKLGSSVTYCHGYVEGTSITLSCIAGDPKPVNNNRPVCTAP 660
Qy      1378 CGGOYVSGDGVLSPNYPOWYTSQOCLVTVVYKDYVVGOGAFHTLNDVVEVHDH 1437
Db      661 CGGOYVSGDGVLSPNYPOWYTSQOCLVTVVYKDYVVGOGAFHTLNDVVEVHDH 720
Qy      1438 SQSRLISLSGSHTESLPLATSNQVLIKFSAGLAPARGFHFVYQAVERTSATOCSSV 1497
Db      721 HAARLLSLSGSHTESLPLATSNQVLIKFSAGLAPARGFHFVYQAVERTSATOCSSV 780
Qy      1498 PEBRYGRLGSDFSVGAIVFECNCGVYALOGSPETLCLPVGALAOVNSAPTCVPCG 1557
Db      781 PEBRYGRLGSDFSVGAIVFECNCGVYALOGSPETLCLPVGALAOVNSAPTCVPCG 840
Qy      1558 NTERGCTILSPRPEYVLSNLCWKIIVPBGAGIOIYVSVFTQNMDSLEVPDGN 1617
Db      841 NTERGCTILSPRPEYVLSNLCWKIIVPBGAGIOIYVSVFTQNMDSLEVPDGN 900
Qy      1618 TVTMLGFSGTVPALINSTSNQLYLHFYSDISVSAAGFLHETKVTGLSCPEPAVPSNG 1677
Db      901 TARLGSFSGTVPALINSTSNQLYLHFYSDISVSAAGFLHETKVTGLSCPEPAVPSNG 960
Qy      1678 VKTGERVLVNDVVSFOCEPGYALOGHAHISCMFGTVARNYPPPLCIAOCGTVBEMEGV 1737
Db      961 IKIGRVMVNDVVSFOCEPGYALOGHAHISCMFGTVARNYPPPLCIAOCGTVBEMEGV 1020
Qy      1738 ILSPPGPNPNMDCGKIALPVGRG 1764
Db      1021 ILSPPGPNPNMDCGKIALPVGRG 1047

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RESULT 15
US-10-016-248-48
; Sequence 48; Application US/10016248
; Publication No. US20040033491A1
; GENERAL INFORMATION:
; APPLICANT: Aleobrook et al.

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; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-218
; CURRENT APPLICATION NUMBER: US/10/016,248
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/254,329
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/291,037
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; PRIOR APPLICATION NUMBER: 60/255,648
; PRIOR FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 60/297,173
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: 60/309,258
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/326,393
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/315,639
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 1043
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-016-248-48

Query Match      24.8%; Score 4209; DB 15; Length 1043;
Best Local Similarity 70.3%; Pred. No. 2,36-292;
Matches 731; Conservative 153; Mismatches 156; Indels 0; Gaps 0;

Qy      725 FHTFHLSEGHVDLITLITENGSPFOPRLQTLGSHLPAPISAGLYGNFTAOVRFISDSMSYE 784
Db      3 FHTFHLSEGHVDLITLITENGSPFOPRLQTLGSHLPAPISAGLYGNFTAOVRFISDSMSYE 62

Qy      785 GNITFSEYDLPECEPEVPAYSIKGLQFGYVDLTFTSCPFPGYLEGTARITICGRRR 844
Db      63 GNITFSEYDLPECEPEVPAYSIKGLQFGYVDLTFTSCPFPGYLEGTARITICGRRR 122

Qy      845 LMSPLPRCAECCGNSVTGCTGTLSPNPNVNNNHETIYSIQOPGKIOLKARFEL 904
Db      123 VMSAPLPRCAECCGNSVTGCTGTLSPNPNVNNNHETIYSIQOPGKIOLKARFEL 182

Qy      905 SEGDVLYKVDGNNNSARLLGVFSHSEMMGVTLNSTSSIMLDPITDAENTSXGFEHFS 964
Db      183 FEGDVLKXYVDGNNNSARLLGVFSHSEMMGVTLNSTSSIMLDPITDAENTSXGFEHFS 242

Qy      965 FELICEDPQTPKFGYKVADEGHFAGSSVSFSCDPGYSLRGSEILLCLSGERRTMDRLP 1024
Db      243 FELICEDPQTPKFGYKVADEGHFAGSSVSFSCDPGYSLRGSEILLCLSGERRTMDRLP 302

Qy      1025 TCVAECGGTVRGEVSGOVLSPGPAVEHNNLCIWTIEAGCTTGLHVLVDTEEVHDV 1084
Db      303 TCVAECGGTVRGEVSGOVLSPGPAVEHNNLCIWTIEAGCTTGLHVLVDTEEVHDV 362

Qy      1085 LRIWDPVSESVLLKELSGPALPKDLSHTFNSVVLQFTDFTSKOGFAIOPSSTATSC 1144
Db      363 LKVMGAPVDSDLILKEMSGALPEDIHSTFNSLTLOPDDFPIKSGFSIORS 422

Qy      1145 NDEGIPONGSRSGDSWEAGDSTVFQCDPGYALOGSAEISCVKIENRFWQSPSPPTCIAC 1204
Db      423 NDEGIPONGSRSGDSWEAGDSTVFQCDPGYALOGSAEISCVKIENRFWQSPSPPTCIAC 482

Qy      1205 GGDLLGPGSVILSPNTPPEYPRGKEDMKVTVSPDVILVFNILFLEPGYD 1264
Db      483 GGDLLGPGSVILSPNTPPEYPRGKEDMKVTVSPDVILVFNILFLEPGYD 542

Qy      1265 DLSPLIGSFYGSQOLPGRIESSNSNLFILAFRSDASVSNAGVIDYTEMNRESCFPDGSIX 1324
Db      543 DLSPLIGSFYGSQOLPGRIESSNSNLFILAFRSDASVSNAGVIDYTEMNRESCFPDGSIX 602

Qy      1325 NSTRVGSDLKLGSSVTYCHGYVEGTSITLSCIAGDPKPVNNNRPVCTAPCGGOYVG 1384
Db      603 NSTRVGSDLKLGSSVTYCHGYVEGTSITLSCIAGDPKPVNNNRPVCTAPCGGOYVG 662

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